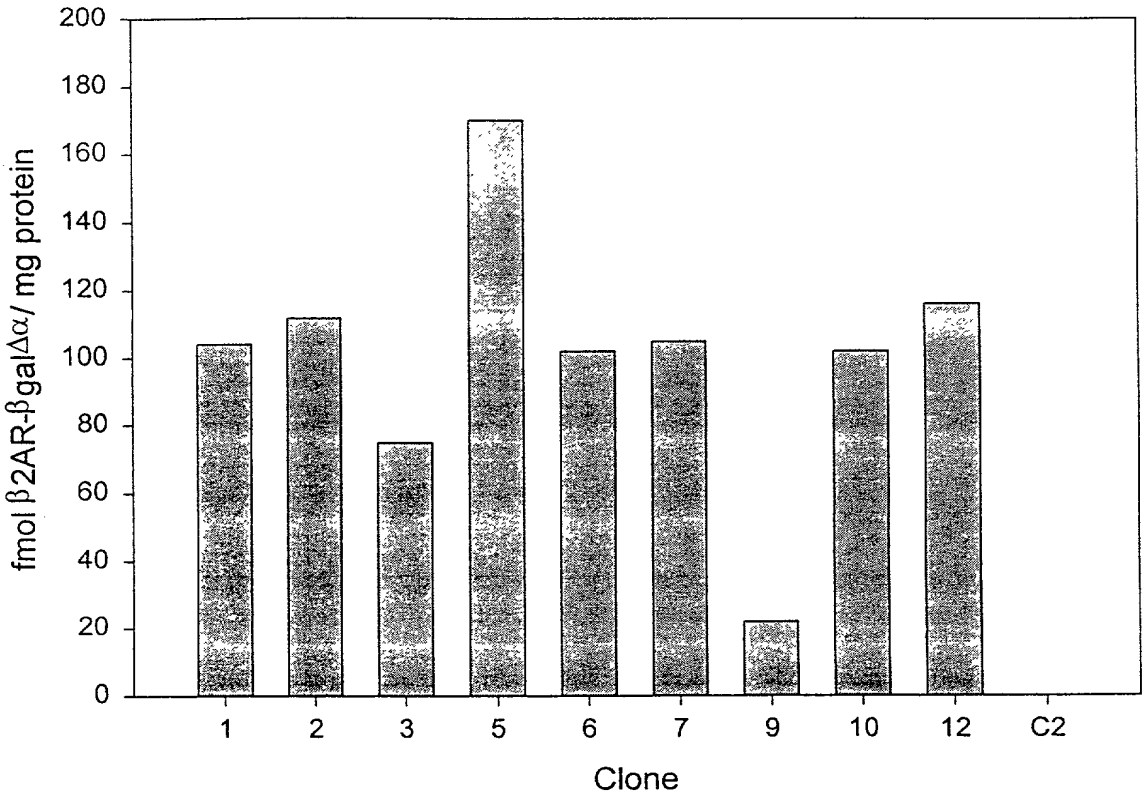
Cellular Expression of β_2AR-βgalΔα Fusion Protein in C2 Clones
(measured by anti-β-gal ELISA)
fmol β2AR-βgalΔα/ mg protein
200
180
160
140
120
100
80
60
40
20
0
1
2
3
5
6
7
9
10
12
C2
Clone

FIGURE 1A

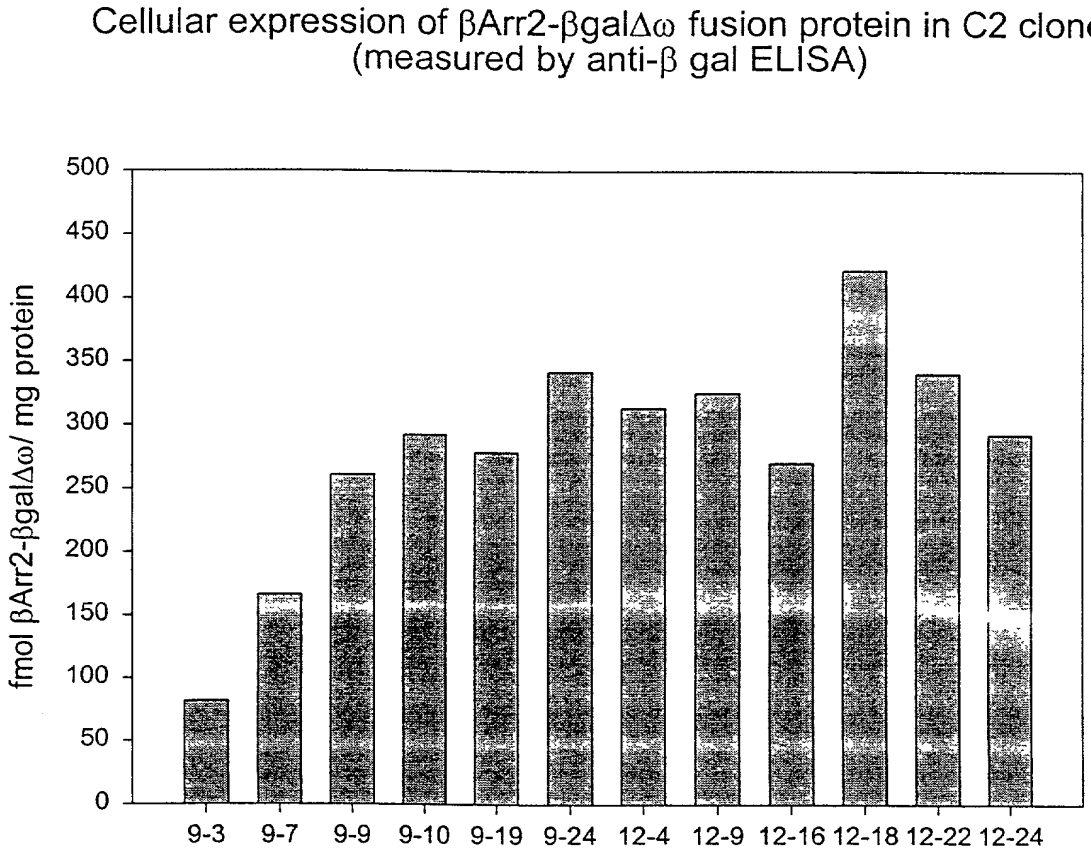
Cellular expression of βArr2-βgalΔω fusion protein in C2 clones
(measured by anti-β gal ELISA)
fmol βArr2-βgalΔω/ mg protein
500
450
400
350
300
250
200
150
100
50
0
9-3
9-7
9-9
9-10
9-19
9-24
12-4
12-9
12-16
12-18
12-22
12-24

FIGURE 1B

Agonist Stimulated cAMP Response in C2 Cells Expressing β2AR-βgalΔα

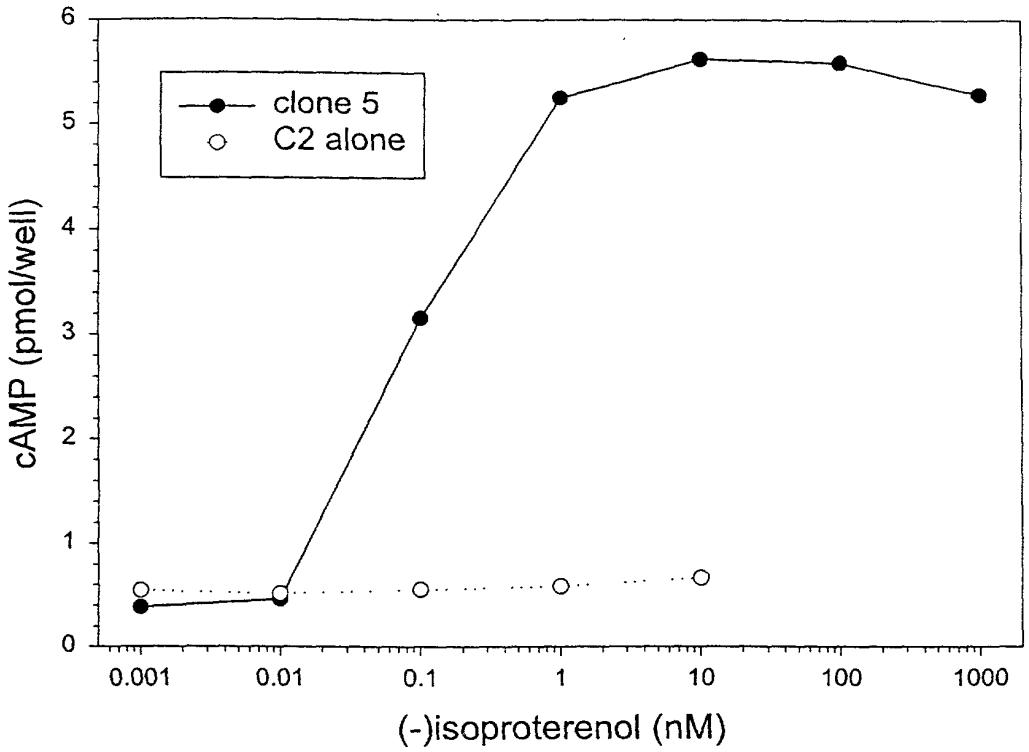

FIGURE 2

β–galactosidase Complementation as a Measurement for β2AR-βgalΔα interacting with βArrestin2-βgalΔω upon agonist Stimulation

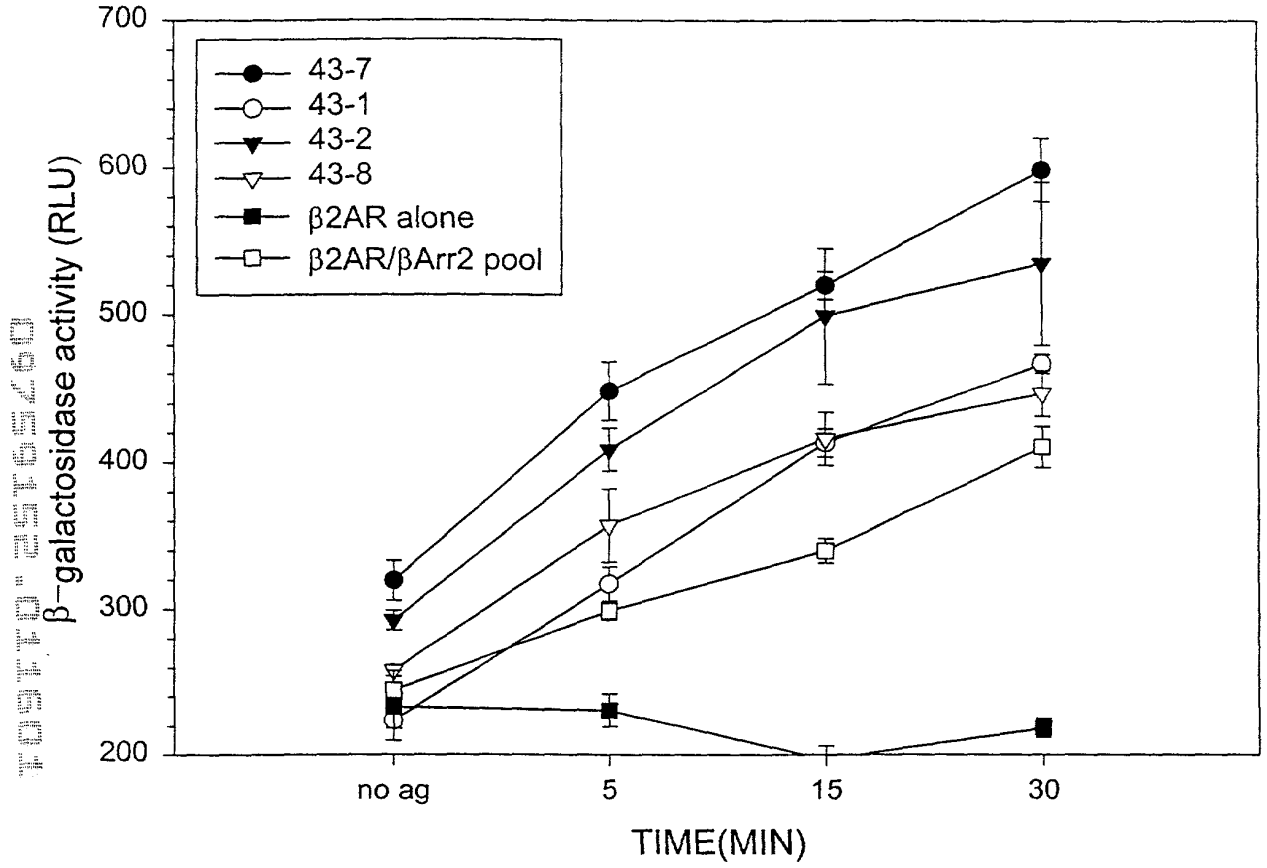

FIGURE 3A

β–galactosidase Complementation as a Measurement for β2AR-βgalΔα Interaction with βArrestin1-βgalΔω upon Agonist Stimulation

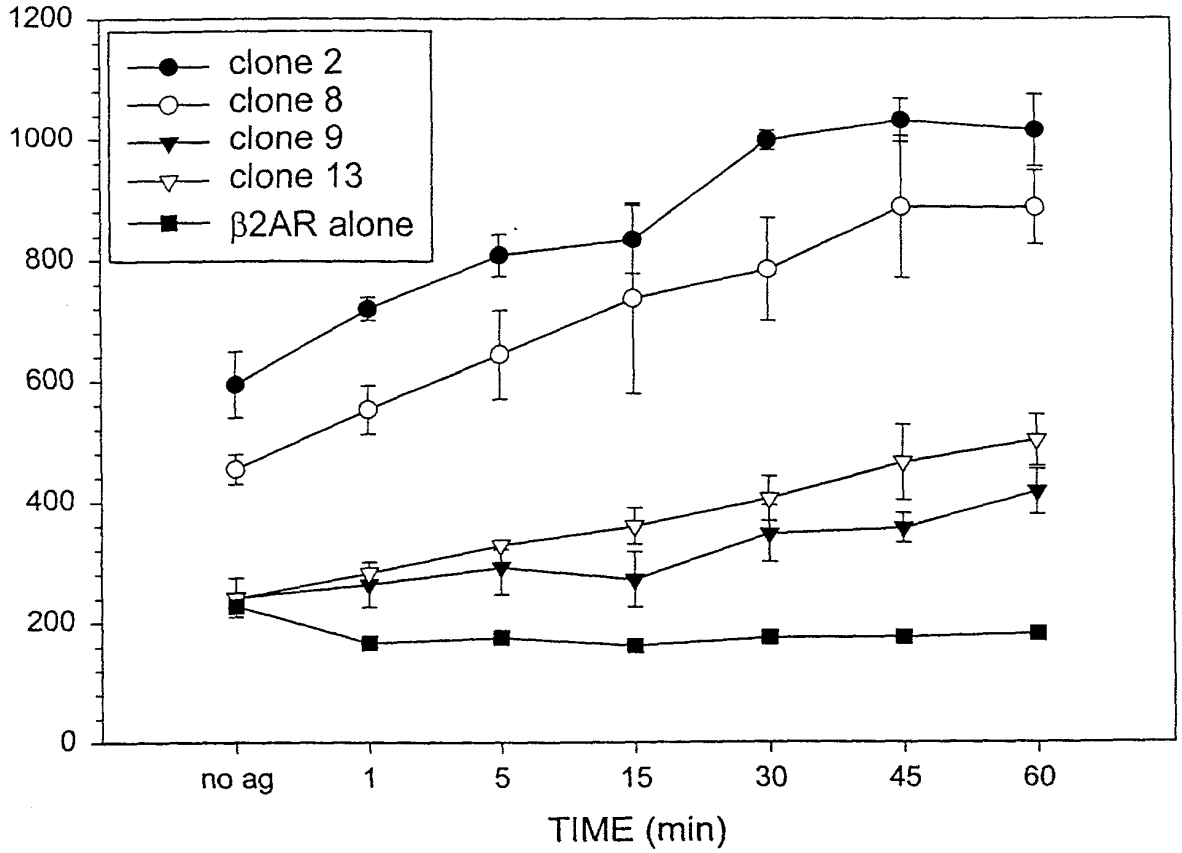

FIGURE 3B

β–galactosidase Activity in Response to Agonist in C2 Cells Coexpressing β2AR-βgalΔα and βArrestin2-βgalΔω Fusion Proteins

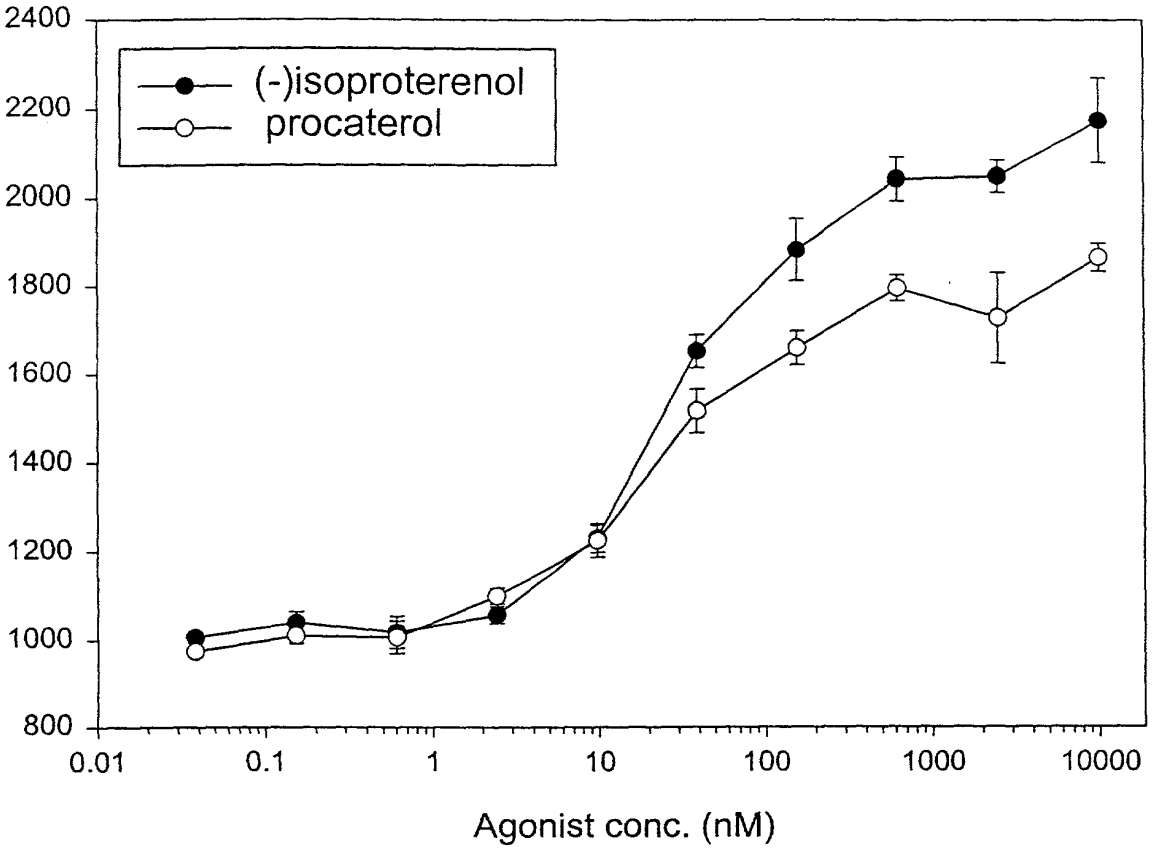

FIGURE 4A

β–galactosidase Activity in Response to Agonist in C2 Cells Coexpressing β2AR-βgalΔα and βArrestin1-βgalΔω Fusion Proteins

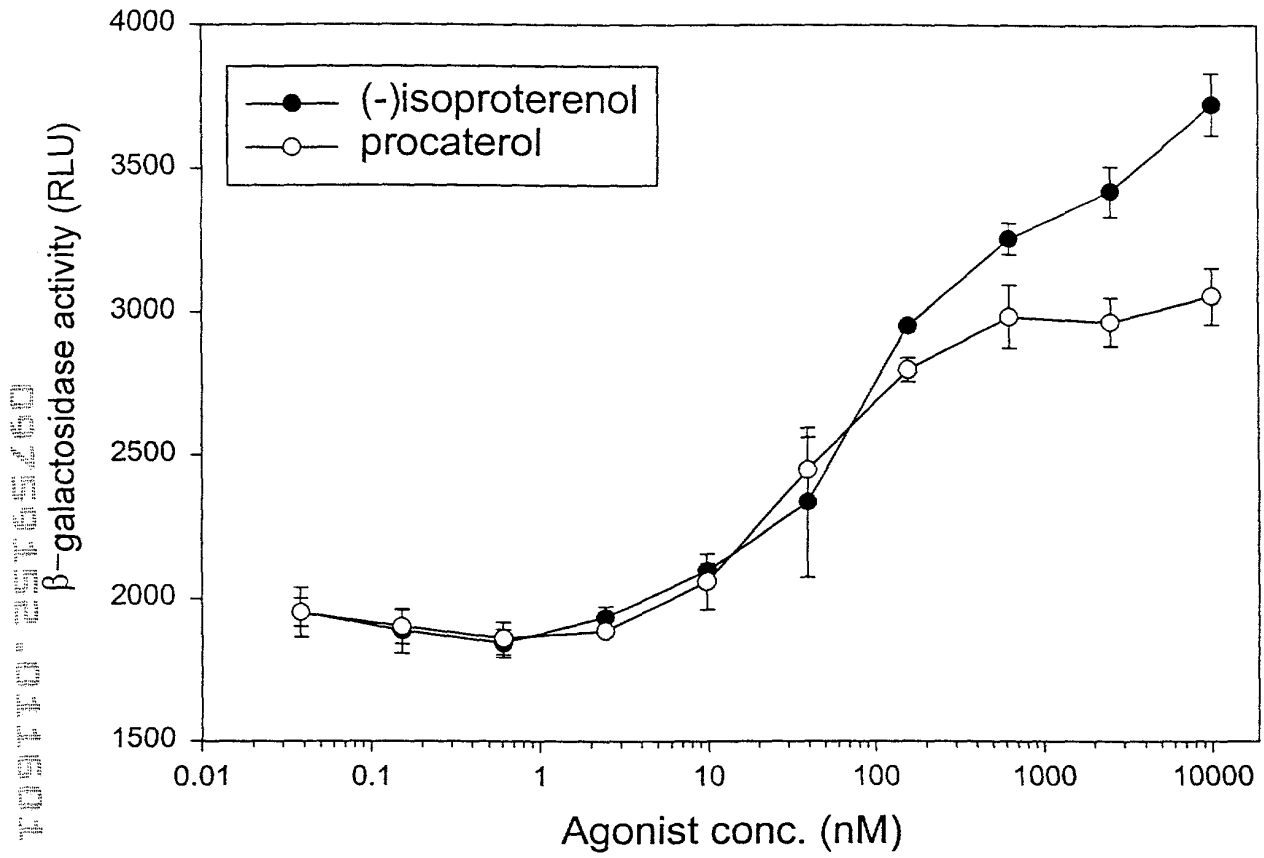

FIGURE 4B

Inhibition of β–galactosidase activity in C2 Cells Coexpressing β2AR–βgalΔα and βArrestin2-βgalΔω Fusion Proteins

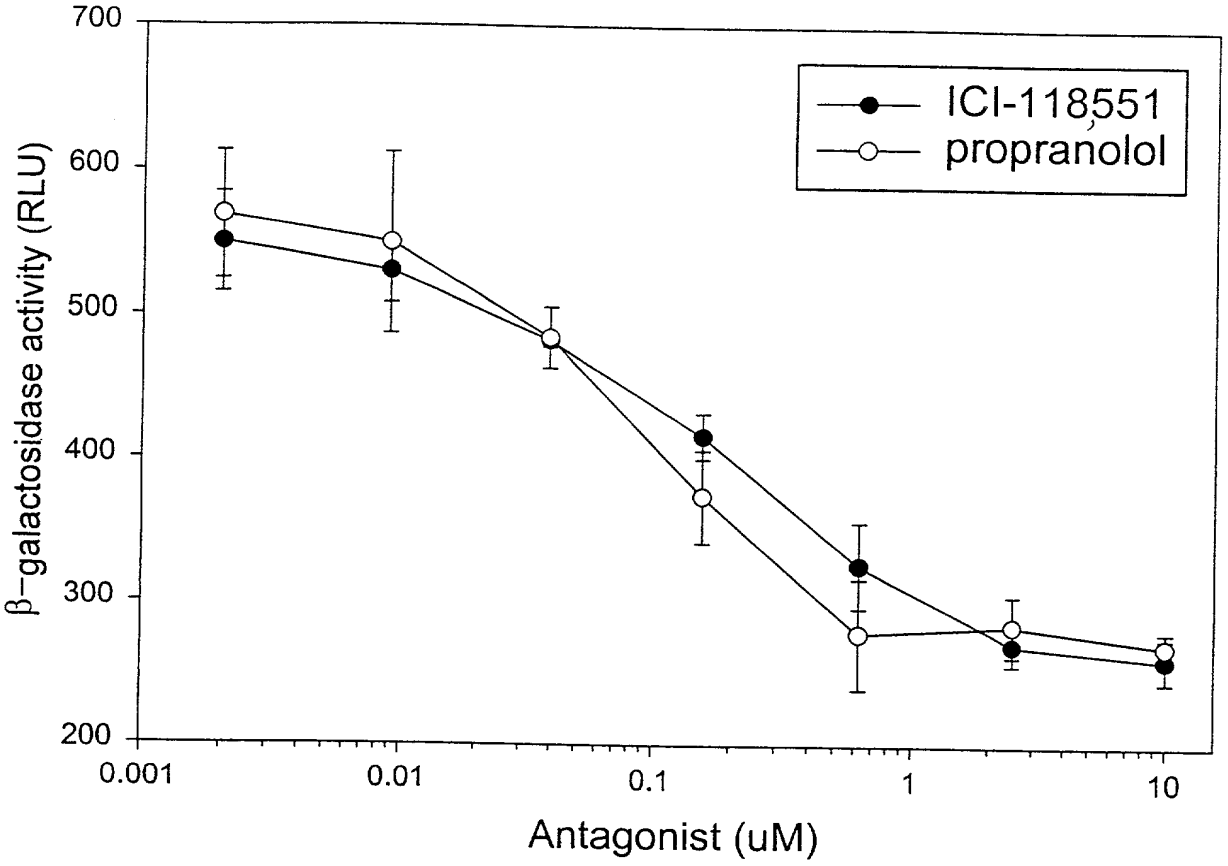

FIGURE 5A

Antagonist Inhibition of β–galactosidase Activity in C2 Cells Coexpressing β2AR-βgalΔα and βArrestin1-βgalΔω Fusion Proteins

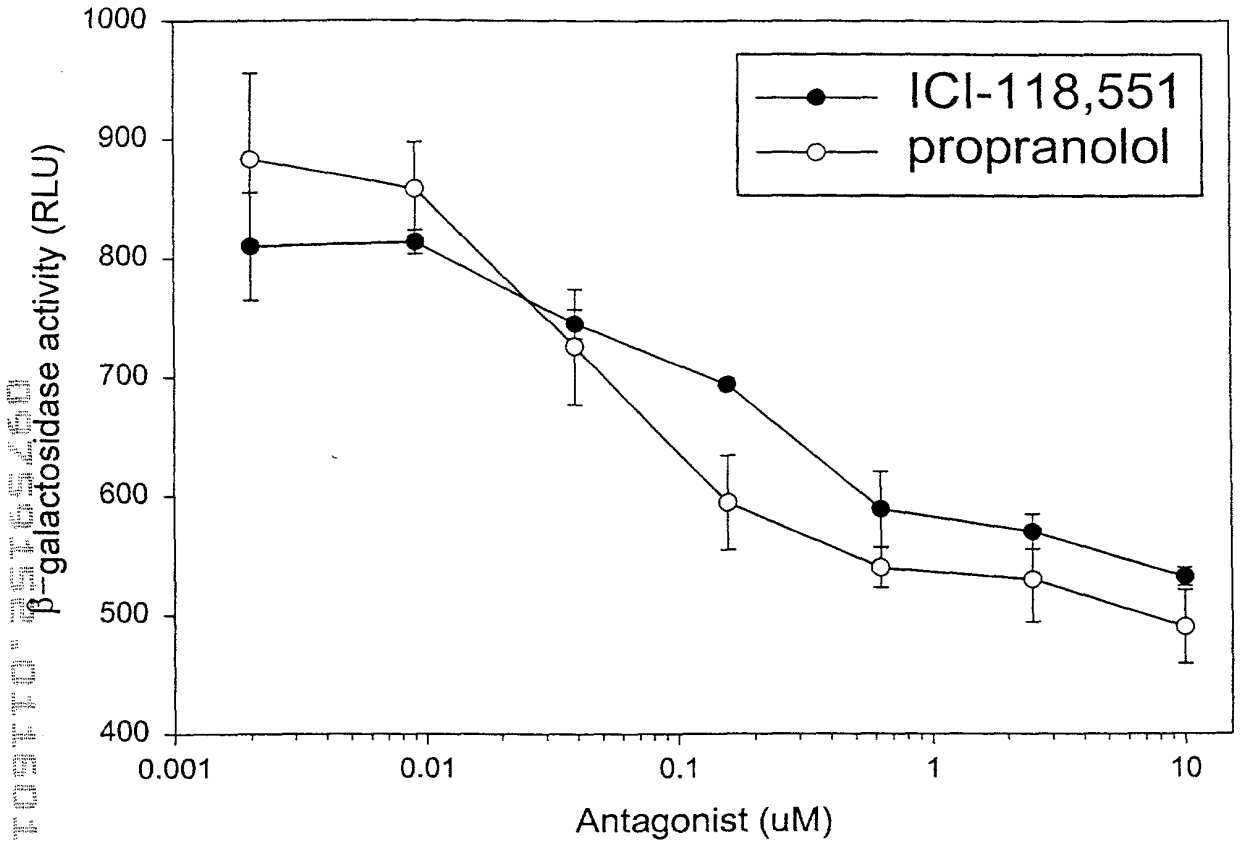

Figure 5B

Agonist Stimulated cAMP Response in Clones or Pools of C2 Cells Coexpressing A2aR-βgalΔα and βArrestin1-βgalΔω Fusion Proteins

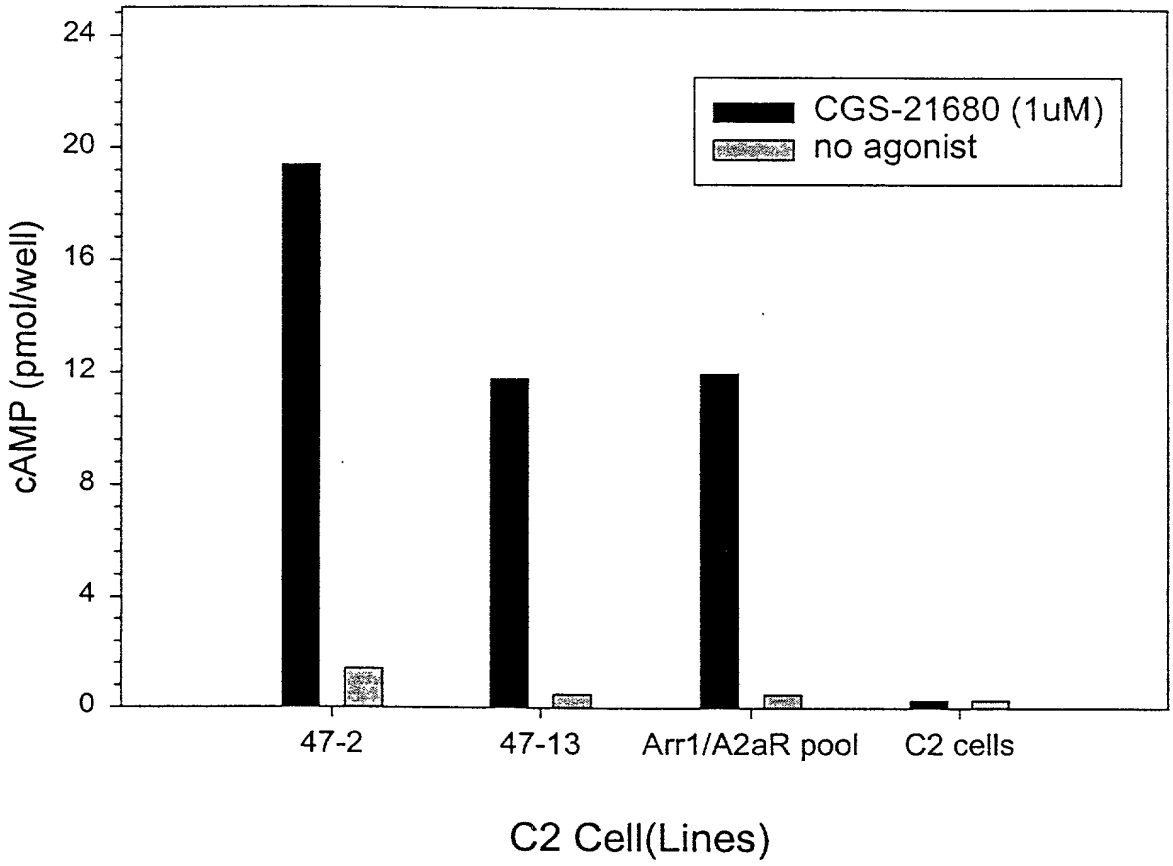

FIGURE 6

Agonist Stimulated cAMP Response in Clones or Pools of C2 Cells Expressing D1-βgalΔα and βArrestin2-βgalΔω Fusion Proteins

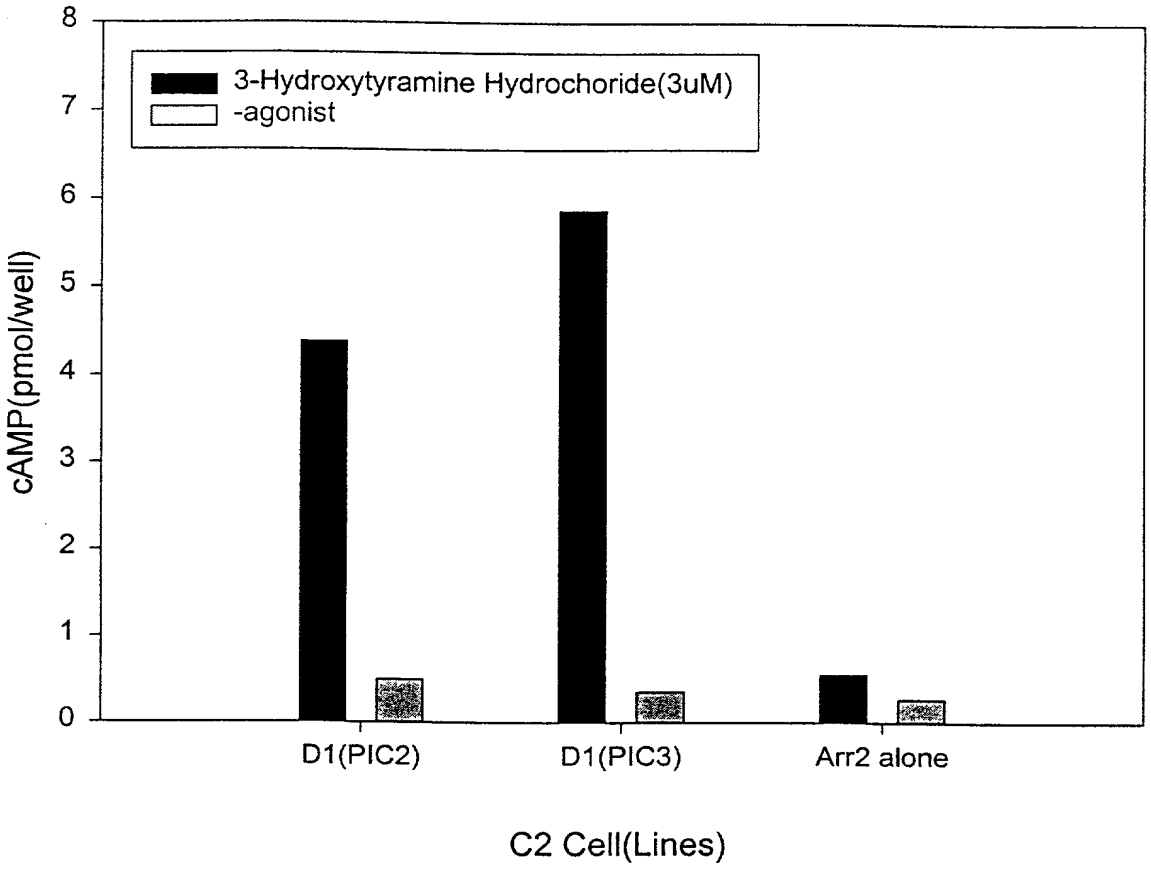

FIGURE 7

β_2AR-βgalΔω and βarr2-βgalΔα Interaction in HEK293 Clones in Response to Isoproterenol Treatment (1 μM)

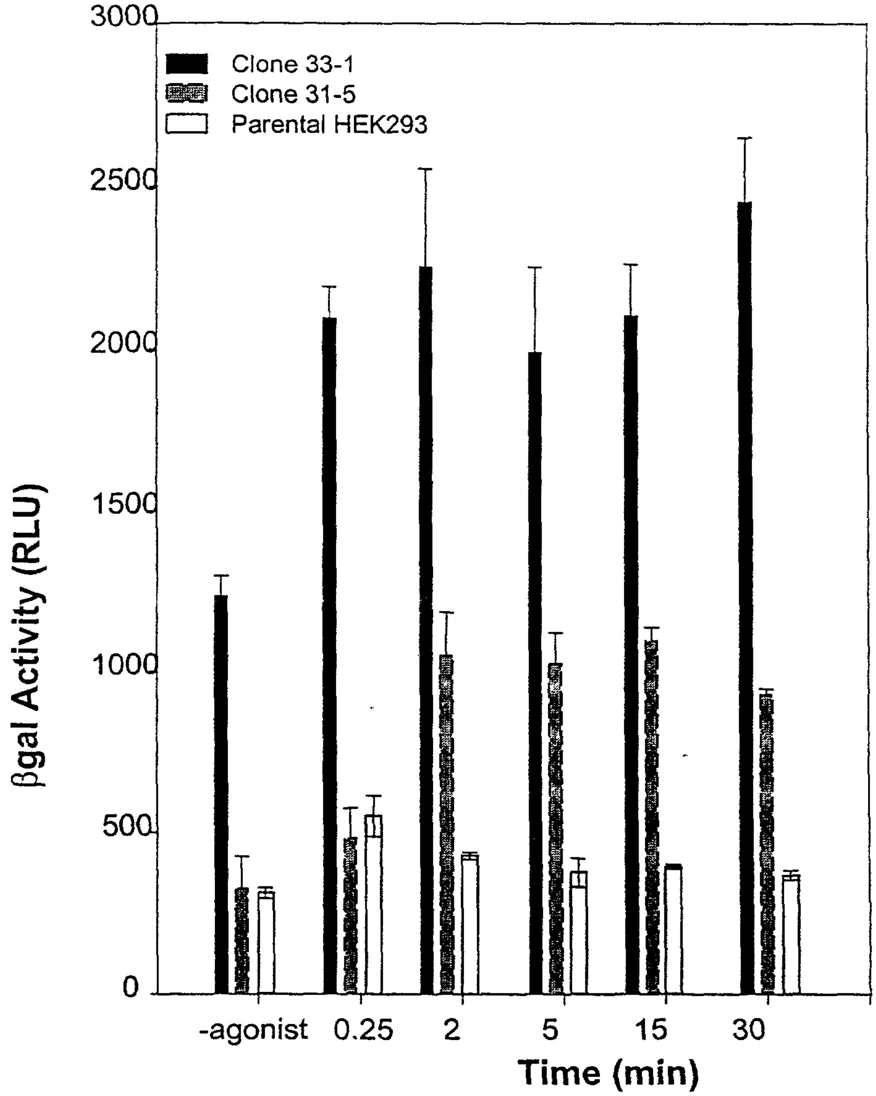

FIGURE 8A

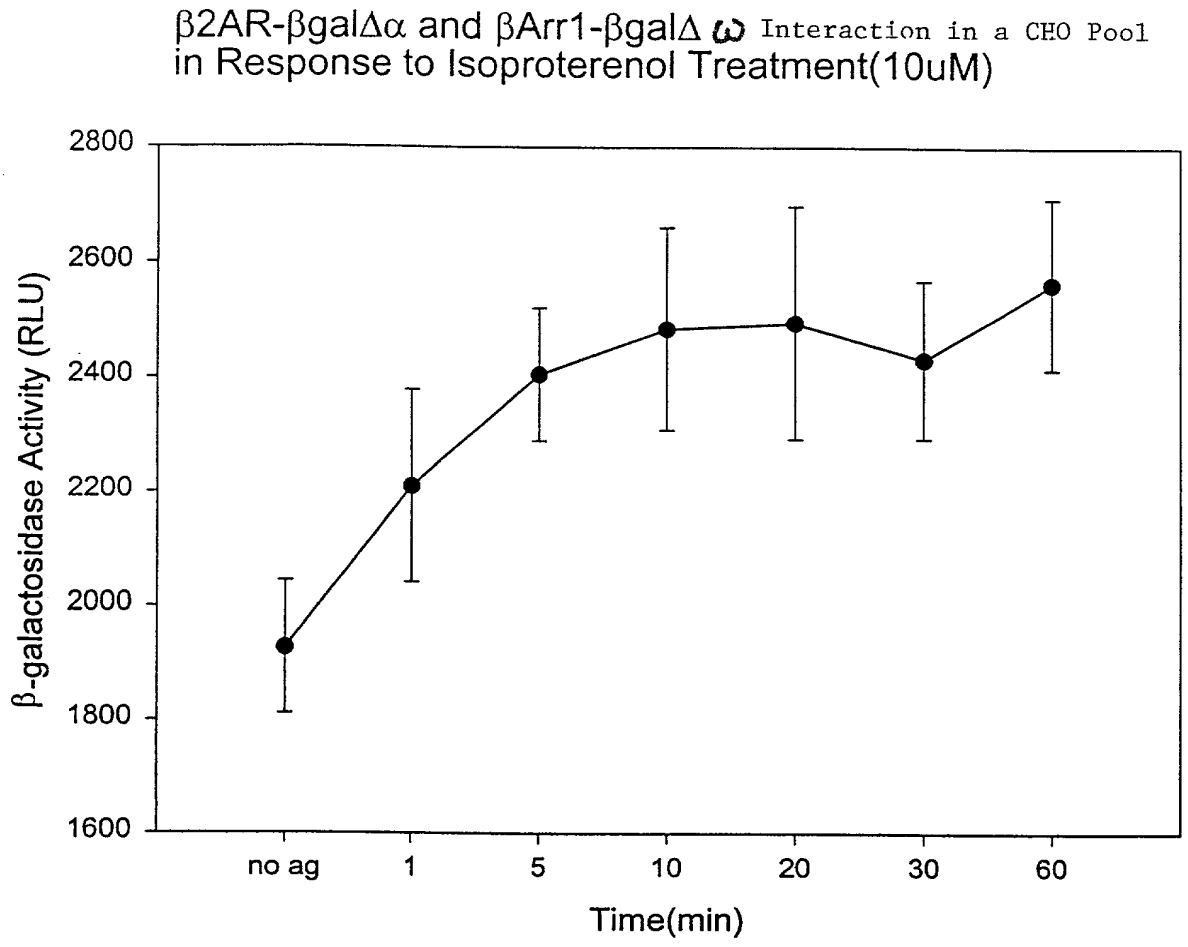
β2AR-βgalΔα and βArr1-βgalΔω Interaction in a CHO Pool
in Response to Isoproterenol Treatment(10uM)
β-galactosidase Activity (RLU)
2800
2600
2400
2200
2000
1800
1600
no ag
1
5
10
20
30
60
Time(min)

FIGURE 8B

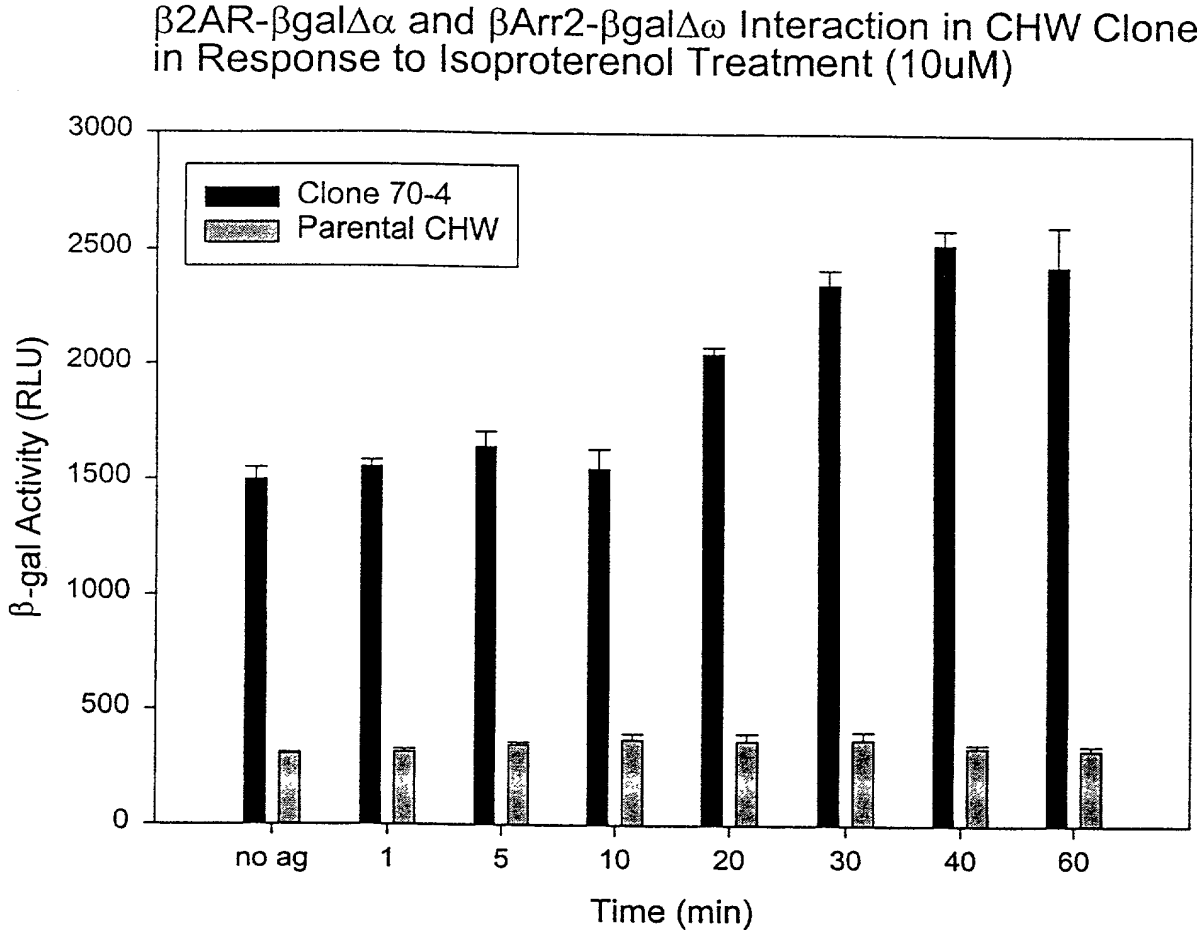
β2AR-βgalΔα and βArr2-βgalΔω Interaction in CHW Clone in Response to Isoproterenol Treatment (10uM)
Clone 70-4
Parental CHW
β-gal Activity (RLU)
3000
2500
2000
1500
1000
500
0
no ag
1
5
10
20
30
40
60
Time (min)

FIGURE 8C

β–galactosidase Complementation as a Measurement for Adrenergic Receptor Homodimerization in HEK 293 Cells Coexpressing β2AR-βgalΔα and β2AR-βgalΔω.

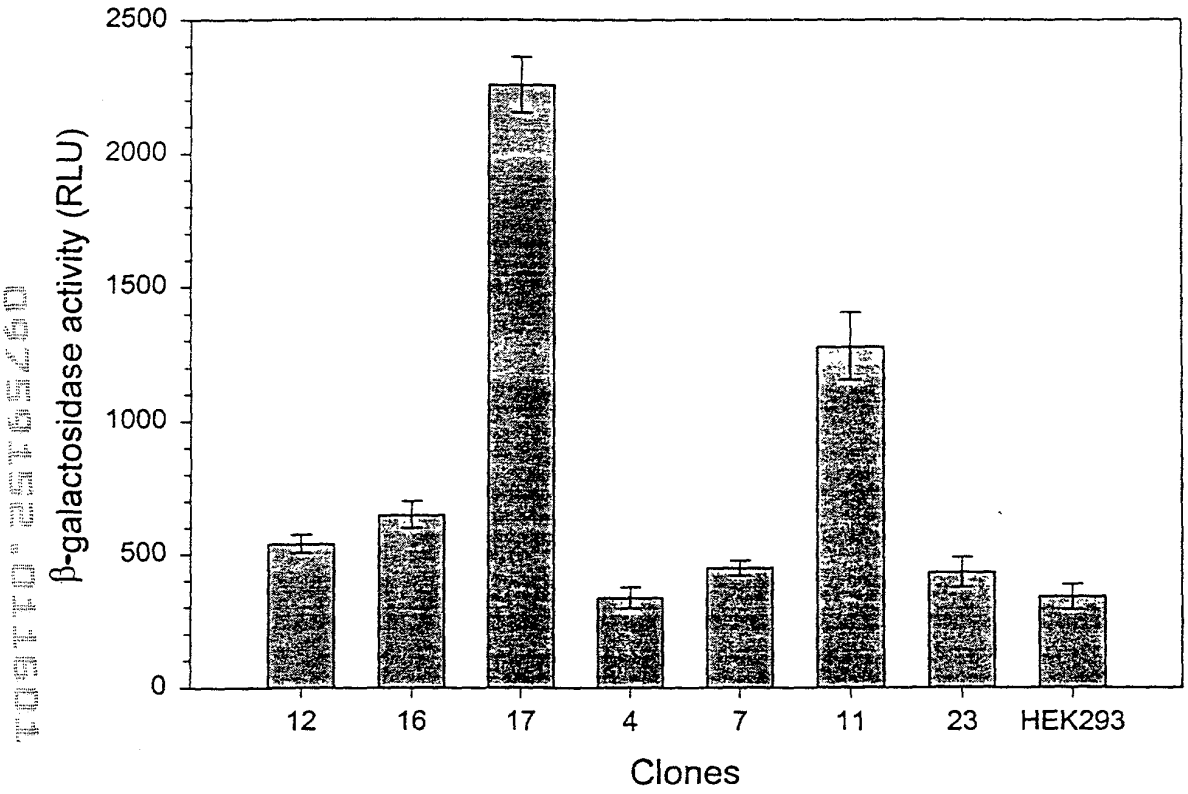

FIGURE 9A

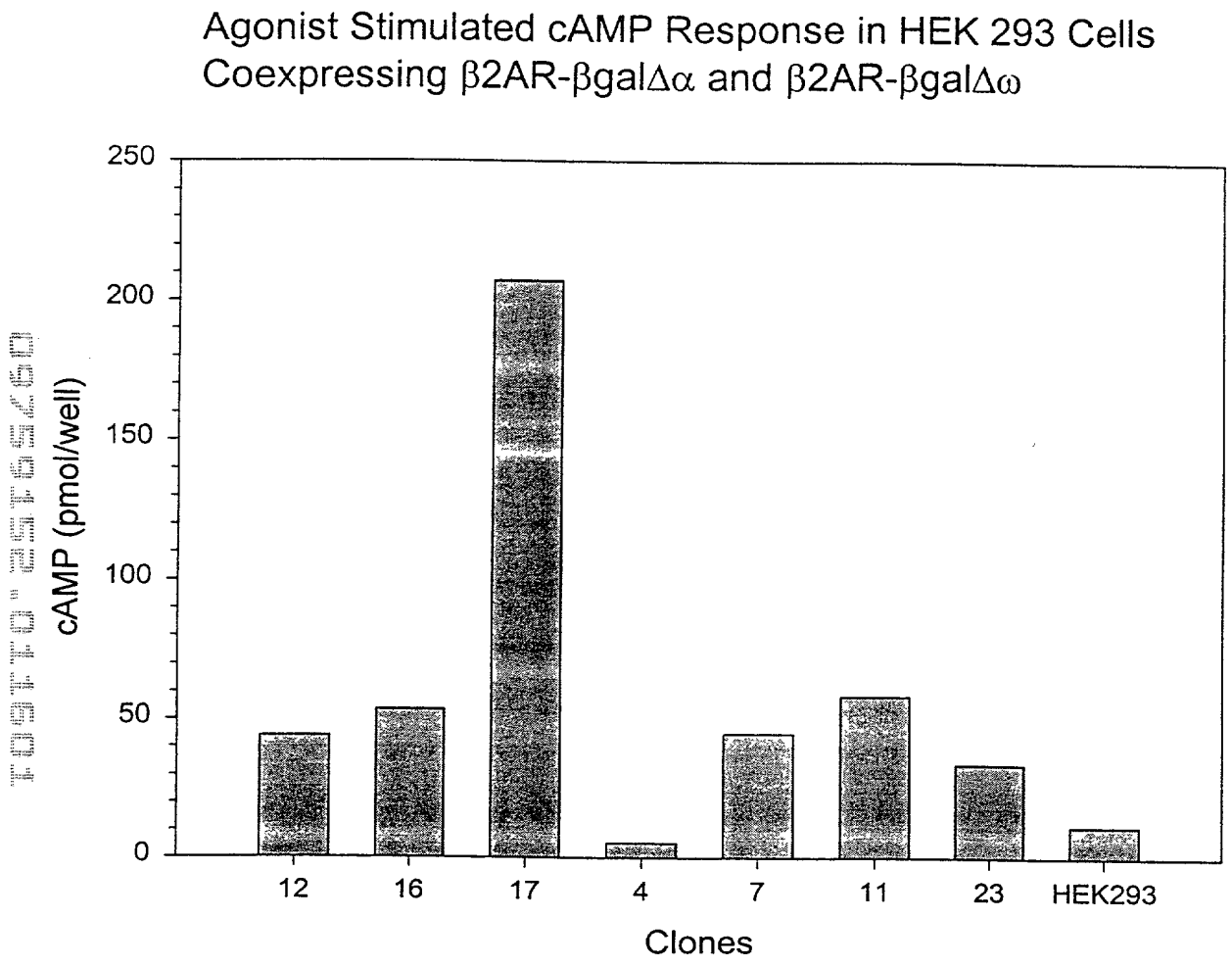
Agonist Stimulated cAMP Response in HEK 293 Cells
Coexpressing β2AR-βgalΔα and β2AR-βgalΔω
cAMP (pmol/well)
250
200
150
100
50
0
12
16
17
4
7
11
23
HEK293
Clones

FIGURE 9B

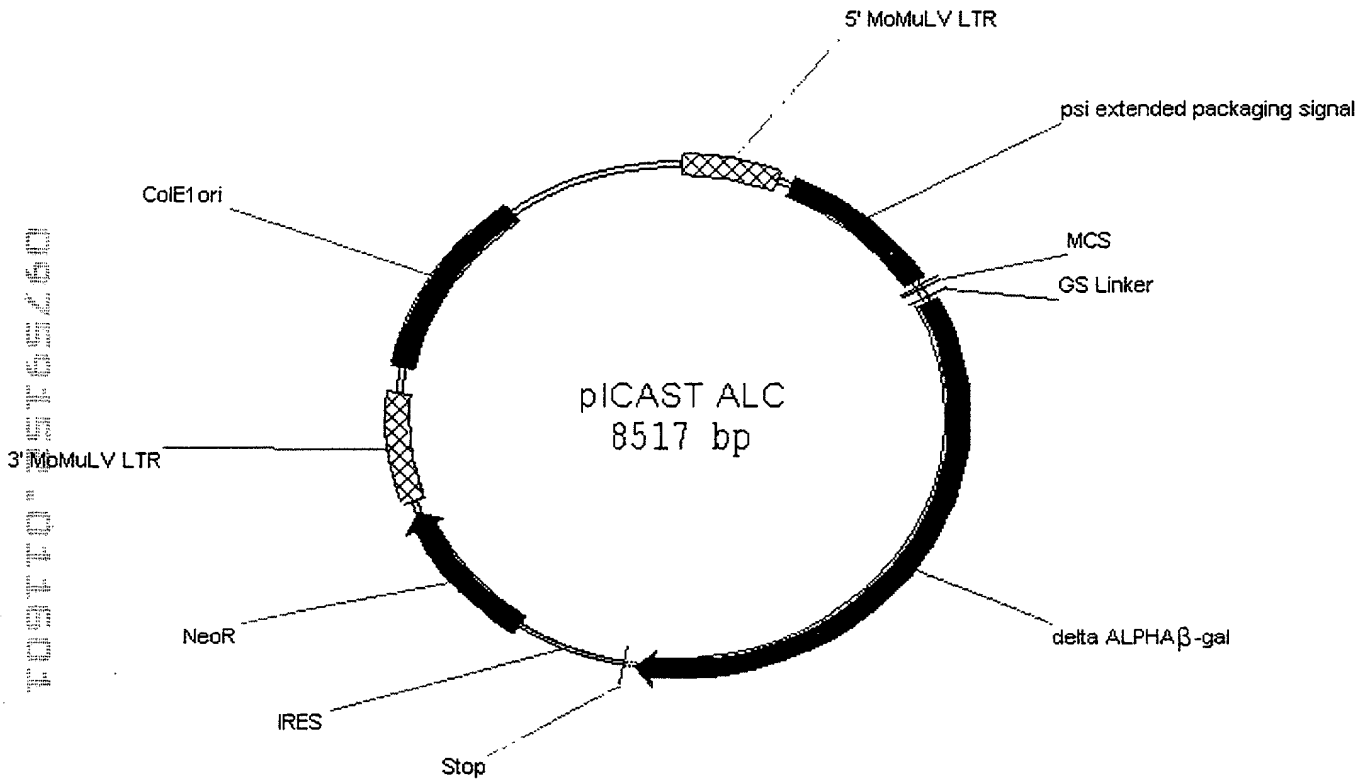
5' MoMuLV LTR
psi extended packaging signal
ColE1 ori
MCS
GS Linker
pICAST ALC
8517 bp
3' MoMuLV LTR
NeoR
delta ALPHAβ-gal
IRES
Stop

Figure 10A

```
  1  CTGCAGCCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG
     GACGTCGGAC TTATACCCGG TTTGTCCTAT AGACACCATT CGTCAAGGAC
---------------------------------------------------------------------------
 51  CCCCGGCTCA GGGCCAAGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA
     GGGGCCGAGT CCCGGTTCTT GTCTACCTTG TCGACTTATA CCCGGTTTGT
---------------------------------------------------------------------------
101  GGATATCTGT GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT
     CCTATAGACA CCATTCGTCA AGGACGGGGC CGAGTCCCGG TTCTTGTCTA
---------------------------------------------------------------------------
151  GGTCCCCAGA TGCGGTCCAG CCCTCAGCAG TTTCTAGAGA ACCATCAGAT
     CCAGGGGTCT ACGCCAGGTC GGGAGTCGTC AAAGATCTCT TGGTAGTCTA
---------------------------------------------------------------------------
201  GTTTCCAGGG TGCCCCAAGG ACCTGAAATG ACCCTGTGCC TTATTTGAAC
     CAAAGGTCCC ACGGGGTTCC TGGACTTTAC TGGGACACGG AATAAACTTG
---------------------------------------------------------------------------
251  TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC TGCTCCCCGA
     ATTGGTTAGT CAAGCGAAGA GCGAAGACAA GCGCGCGAAG ACGAGGGGCT
---------------------------------------------------------------------------
301  GCTCAATAAA AGAGCCCACA ACCCCTCACT CGGGGCGCCA GTCCTCCGAT
     CGAGTTATTT TCTCGGGTGT TGGGGAGTGA GCCCCGCGGT CAGGAGGCTA
---------------------------------------------------------------------------
351  TGACTGAGTC GCCCGGGTAC CCGTGTATCC AATAAACCCT CTTGCAGTTG
     ACTGACTCAG CGGGCCCATG GCCACATAGG TTATTTGGGA GAACGTCAAC
---------------------------------------------------------------------------
401  CATCCGACTT GTGGTCTCGC TGTTCCTTGG GAGGGTCTCC TCTGAGTGAT
     GTAGGCTGAA CACCAGAGCG ACAAGGAACC CTCCCAGAGG AGACTCACTA
---------------------------------------------------------------------------
451  TGACTACCCG TCAGCGGGGG TCTTTCATTT GGGGGCTCGT CCGGGATCGG
     ACTGATGGGC AGTCGCCCCC AGAAAGTAAA CCCCCGAGCA GGCCCTAGCC
---------------------------------------------------------------------------
501  GAGACCCCTG CCCAGGGACC ACCGACCCAC CACCGGGAGG CAAGCTGGCC
     CTCTGGGGAC GGGTCCCTGG TGGCTGGGTG GTGGCCCTCC GTTCGACCGG
---------------------------------------------------------------------------
551  AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG ACTGATTTTA
     TCGTTGAATA GACACAGACA GGCTAACAGA TCACAGATAC TGACTAAAAT
---------------------------------------------------------------------------
601  TGCGCCTGCG TCGGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC
     ACGCGGACGC AGCCATGATC AATCGATTGA TCGAGACATA GACCGCCTGG
---------------------------------------------------------------------------
651  CGTGGTGGAA CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG
     GCACCACCTT GACTGCTCAA GACTTGTGGG CCGGCGTTGG GACCCTCTGC
---------------------------------------------------------------------------
701  TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG CCCGACCTGA GGAAGGGAGT
     AGGGTCCCTG AAACCCCCGG CAAAAACACC GGGCTGGACT CCTTCCCTCA
---------------------------------------------------------------------------
751  CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT AGGAGACGAG
     GCTACACCTT AGGCTGGGGC AGTCCTATAC ACCAAGACCA TCCTCTGCTC
---------------------------------------------------------------------------
801  AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA
     TTGGATTTTG TCAAGGGCGG AGGCAGACTT AAAAACGAAA GCCAAACCTT
---------------------------------------------------------------------------
851  CCGAAGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT
     GGCTTCGGCG CGCAGAACAG ACGACGTCGT AGCAAGACAC AACAGAGACA
---------------------------------------------------------------------------
901  CTGACTGTGT TTCTGTATTT GTCTGAAAAT TAGGGCCAGA CTGTTACCAC
     GACTGACACA AAGACATAAA CAGACTTTTA ATCCCGGTCT GACAATGGTG
---------------------------------------------------------------------------
```

FIGURE 10B

```
 951  TCCCTTAAGT TTCACCTTAG GTAACTGGAA AGATGTCGAG CGGCTCGCTC
      AGGGAATTCA AACTGGAATC CATTGACCTT TCTACAGCTC GCCGAGCGAG
-------------------------------------------------------------------------------

1001  ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
      TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
-------------------------------------------------------------------------------

1051  GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
      CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
-------------------------------------------------------------------------------

1101  CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
      GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
-------------------------------------------------------------------------------

1151  ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
      TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
-------------------------------------------------------------------------------

1201  TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
      AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
-------------------------------------------------------------------------------

1251  TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
      AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
-------------------------------------------------------------------------------

1301  CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
      GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
-------------------------------------------------------------------------------

1351  GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAATCAGG
      CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTAGTCC
-------------------------------------------------------------------------------

1401  CCTTGGCGCG CCGGATCCTT AATTAAGCGC AATTGGGAGG TGGCGGTAGC
      GGAACCGCGC GGCCTAGGAA TTAATTCGCG TTAACCCTCC ACCGCCATCG
-------------------------------------------------------------------------------

 +2         M  G   V  I  T   D  S  L   A  V  V  A   R  T  D
           ]-------------------------------------------------
1451  CTCGAGATGG GCGTGATTAC GGATTCACTG GCCGTCGTGG CCCGCACCGA
      GAGCTCTACC CGCACTAATG CCTAAGTGAC CGGCAGCACC GGGCGTGGCT
-------------------------------------------------------------------------------

  +2   R  P  S   Q  Q  L  R   S  L  N   G  E  W   R  F  A
       ---------------------------------------------------
1501  TCGCCCTTCC CAACAGTTAC GCAGCCTGAA TGGCGAATGG CGCTTTGCCT
      AGCGGGAAGG GTTGTCAATG CGTCGGACTT ACCGCTTACC GCGAAACGGA
-------------------------------------------------------------------------------

  +2 W  F  P  A   P  E  A   V  P  E  S   W  L  E   C  D  L
     ---------------------------------------------------
1551  GGTTTCCGGC ACCAGAAGCG GTGCCGGAAA GCTGGCTGGA GTGCGATCTT
      CCAAAGGCCG TGGTCTTCGC CACGGCCTTT CGACCGACCT CACGCTAGAA
-------------------------------------------------------------------------------

  +2  P  E  A  D   T  V  V   V  P  S   N  W  Q  M   H  G  Y
      ---------------------------------------------------
1601  CCTGAGGCCG ATACTGTCGT CGTCCCCTCA AACTGGCAGA TGCACGGTTA
      GGACTCCGGC TATGACAGCA GCAGGGGAGT TTGACCGTCT ACGTGCCAAT
-------------------------------------------------------------------------------

  +2   D  A  P   I  Y  T  N   V  T  Y   P  I  T   V  N  P
       ---------------------------------------------------
1651  CGATGCGCCC ATCTACACCA ACGTGACCTA TCCCATTACG GTCAATCCGC
      GCTACGCGGG TAGATGTGGT TGCACTGGAT AGGGTAATGC CAGTTAGGCG
-------------------------------------------------------------------------------
```

```
   +2 P  F  V  P  T  E  N  P  T  G  C  Y  S  L  T  F  N
      ----------------------------------------------------
1701  CGTTTGTTCC CACGGAGAAT CCGACGGGTT GTTACTCGCT CACATTTAAT
      GCAAACAAGG GTGCCTCTTA GGCTGCCCAA CAATGAGCGA GTGTAAATTA
-------------------------------------------------------------------------------
   +2 V  D  E  S  W  L  Q  E  G  Q  T  R  I  I  F  D  G
      ----------------------------------------------------
1751  GTTGATGAAA GCTGGCTACA GGAAGGCCAG ACGCGAATTA TTTTTGATGG
      CAACTACTTT CGACCGATGT CCTTCCGGTC TGCGCTTAAT AAAAACTACC
-------------------------------------------------------------------------------
   +2  V  N  S  A  F  H  L  W  C  N  G  R  W  V  G  Y
      ----------------------------------------------------
1801  CGTTAACTCG GCGTTTCATC TGTGGTGCAA CGGGCGCTGG GTCGGTTACG
      GCAATTGAGC CGCAAAGTAG ACACCACGTT GCCCGCGACC CAGCCAATGC
-------------------------------------------------------------------------------
   +2 G  Q  D  S  R  L  P  S  E  F  D  L  S  A  F  L  R
      ----------------------------------------------------
1851  GCCAGGACAG TCGTTTGCCG TCTGAATTTG ACCTGAGCGC ATTTTTACGC
      CGGTCCTGTC AGCAAACGGC AGACTTAAAC TGGACTCGCG TAAAAATGCG
-------------------------------------------------------------------------------
   +2  A  G  E  N  R  L  A  V  M  V  L  R  W  S  D  G  S
      ----------------------------------------------------
1901  GCCGGAGAAA ACCGCCTCGC GGTGATGGTG CTGCGCTGGA GTGACGGCAG
      CGGCCTCTTT TGGCGGAGCG CCACTACCAC GACGCGACCT CACTGCCGTC
-------------------------------------------------------------------------------
   +2  Y  L  E  D  Q  D  M  W  R  M  S  G  I  F  R  D
      ----------------------------------------------------
1951  TTATCTGGAA GATCAGGATA TGTGGCGGAT GAGCGGCATT TTCCGTGACG
      AATAGACCTT CTAGTCCTAT ACACCGCCTA CTCGCCGTAA AAGGCACTGC
-------------------------------------------------------------------------------
   +2 V  S  L  L  H  K  P  T  T  Q  I  S  D  F  H  V  A
      ----------------------------------------------------
2001  TCTCGTTGCT GCATAAACCG ACTACACAAA TCAGCGATTT CCATGTTGCC
      AGAGCAACGA CGTATTTGGC TGATGTGTTT AGTCGCTAAA GGTACAACGG
-------------------------------------------------------------------------------
   +2  T  R  F  N  D  D  F  S  R  A  V  L  E  A  E  V  Q
      ----------------------------------------------------
2051  ACTCGCTTTA ATGATGATTT CAGCCGCGCT GTACTGGAGG CTGAAGTTCA
      TGAGCGAAAT TACTACTAAA GTCGGCGCGA CATGACCTCC GACTTCAAGT
-------------------------------------------------------------------------------
   +2  M  C  G  E  L  R  D  Y  L  R  V  T  V  S  L  W
      ----------------------------------------------------
2101  GATGTGCGGC GAGTTGCGTG ACTACCTACG GGTAACAGTT TCTTTATGGC
      CTACACGCCG CTCAACGCAC TGATGGATGC CCATTGTCAA AGAAATACCG
-------------------------------------------------------------------------------
   +2 Q  G  E  T  Q  V  A  S  G  T  A  P  F  G  G  E  I
      ----------------------------------------------------
2151  AGGGTGAAAC GCAGGTCGCC AGCGGCACCG CGCCTTTCGG CGGTGAAATT
      TCCCACTTTG CGTCCAGCGG TCGCCGTGGC GCGGAAAGCC GCCACTTTAA
-------------------------------------------------------------------------------
   +2  I  D  E  R  G  G  Y  A  D  R  V  T  L  R  L  N  V
      ----------------------------------------------------
2201  ATCGATGAGC GTGGTGGTTA TGCCGATCGC GTCACACTAC GTCTGAACGT
      TAGCTACTCG CACCACCAAT ACGGCTAGCG CAGTGTGATG CAGACTTGCA
-------------------------------------------------------------------------------
   +2  E  N  P  K  L  W  S  A  E  I  P  N  L  Y  R  A
      ----------------------------------------------------
2251  CGAAAACCCG AAACTGTGGA GCGCCGAAAT CCCGAATCTC TATCGTGCGG
      GCTTTTGGGC TTTGACACCT CGCGGCTTTA GGGCTTAGAG ATAGCACGCC
-------------------------------------------------------------------------------
```

```
   +2 V  V  E  L  H  T  A  D  G  T  L  I  E  A  E  A  C
      ----------------------------------------------------
2301  TGGTTGAACT GCACACCGCC GACGGCACGC TGATTGAAGC AGAAGCCTGC
      ACCAACTTGA CGTGTGGCGG CTGCCGTGCG ACTAACTTCG TCTTCGGACG
 ------------------------------------------------------------------------------------------

   +2  D  V  G  F  R  E  V  R  I  E  N  G  L  L  L  L  N
      ----------------------------------------------------
2351  GATGTCGGTT TCCGCGAGGT GCGGATTGAA AATGGTCTGC TGCTGCTGAA
      CTACAGCCAA AGGCGCTCCA CGCCTAACTT TTACCAGACG ACGACGACTT
 ------------------------------------------------------------------------------------------

   +2   G  K  P  L  L  I  R  G  V  N  R  H  E  H  H  P
      ----------------------------------------------------
2401  CGGCAAGCCG TTGCTGATTC GAGGCGTTAA CCGTCACGAG CATCATCCTC
      GCCGTTCGGC AACGACTAAG CTCCGCAATT GGCAGTGCTC GTAGTAGGAG
 ------------------------------------------------------------------------------------------

   +2 L  H  G  Q  V  M  D  E  Q  T  M  V  Q  D  I  L  L
      ----------------------------------------------------
2451  TGCATGGTCA GGTCATGGAT GAGCAGACGA TGGTGCAGGA TATCCTGCTG
      ACGTACCAGT CCAGTACCTA CTCGTCTGCT ACCACGTCCT ATAGGACGAC
 ------------------------------------------------------------------------------------------

   +2  M  K  Q  N  N  F  N  A  V  R  C  S  H  Y  P  N  H
      ----------------------------------------------------
2501  ATGAAGCAGA ACAACTTTAA CGCCGTGCGC TGTTCGCATT ATCCGAACCA
      TACTTCGTCT TGTTGAAATT GCGGCACGCG ACAAGCGTAA TAGGCTTGGT
 ------------------------------------------------------------------------------------------

   +2   P  L  W  Y  T  L  C  D  R  Y  G  L  Y  V  V  D
      ----------------------------------------------------
2551  TCCGCTGTGG TACACGCTGT GCGACCGCTA CGGCCTGTAT GTGGTGGATG
      AGGCGACACC ATGTGCGACA CGCTGGCGAT GCCGGACATA CACCACCTAC
 ------------------------------------------------------------------------------------------

   +2 E  A  N  I  E  T  H  G  M  V  P  M  N  R  L  T  D
      ----------------------------------------------------
2601  AAGCCAATAT TGAAACCCAC GGCATGGTGC CAATGAATCG TCTGACCGAT
      TTCGGTTATA ACTTTGGGTG CCGTACCACG GTTACTTAGC AGACTGGCTA
 ------------------------------------------------------------------------------------------

   +2  D  P  R  W  L  P  A  M  S  E  R  V  T  R  M  V  Q
      ----------------------------------------------------
2651  GATCCGCGCT GGCTACCGGC GATGAGCGAA CGCGTAACGC GAATGGTGCA
      CTAGGCGCGA CCGATGGCCG CTACTCGCTT GCGCATTGCG CTTACCACGT
 ------------------------------------------------------------------------------------------

   +2   R  D  R  N  H  P  S  V  I  I  W  S  L  G  N  E
      ----------------------------------------------------
2701  GCGCGATCGT AATCACCCGA GTGTGATCAT CTGGTCGCTG GGGAATGAAT
      CGCGCTAGCA TTAGTGGGCT CACACTAGTA GACCAGCGAC CCCTTACTTA
 ------------------------------------------------------------------------------------------

   +2 S  G  H  G  A  N  H  D  A  L  Y  R  W  I  K  S  V
      ----------------------------------------------------
2751  CAGGCCACGG CGCTAATCAC GACGCGCTGT ATCGCTGGAT CAAATCTGTC
      GTCCGGTGCC GCGATTAGTG CTGCGCGACA TAGCGACCTA GTTTAGACAG
 ------------------------------------------------------------------------------------------

   +2  D  P  S  R  P  V  Q  Y  E  G  G  G  A  D  T  T  A
      ----------------------------------------------------
2801  GATCCTTCCC GCCCGGTGCA GTATGAAGGC GGCGGAGCCG ACACCACGGC
      CTAGGAAGGG CGGGCCACGT CATACTTCCG CCGCCTCGGC TGTGGTGCCG
 ------------------------------------------------------------------------------------------

   +2   T  D  I  I  C  P  M  Y  A  R  V  D  E  D  Q  P
      ----------------------------------------------------
2851  CACCGATATT ATTTGCCCGA TGTACGCGCG CGTGGATGAA GACCAGCCCT
      GTGGCTATAA TAAACGGGCT ACATGCGCGC GCACCTACTT CTGGTCGGGA
 ------------------------------------------------------------------------------------------
```

```
   +2 F  P  A  V  P  K  W  S  I  K  K  W  L  S  L  P  G
      ------------------------------------------------
2901  TCCCGGCTGT GCCGAAATGG TCCATCAAAA AATGGCTTTC GCTACCTGGA
      AGGGCCGACA CGGCTTTACC AGGTAGTTTT TTACCGAAAG CGATGGACCT
------------------------------------------------------------------------------
   +2 E  T  R  P  L  I  L  C  E  Y  A  H  A  M  G  N  S
      ------------------------------------------------
2951  GAGACGCGCC CGCTGATCCT TTGCGAATAC GCCCACGCGA TGGGTAACAG
      CTCTGCGCGG GCGACTAGGA AACGCTTATG CGGGTGCGCT ACCCATTGTC
------------------------------------------------------------------------------
   +2  L  G  G  F  A  K  Y  W  Q  A  F  R  Q  Y  P  R
      ------------------------------------------------
3001  TCTTGGCGGT TTCGCTAAAT ACTGGCAGGC GTTTCGTCAG TATCCCCGTT
      AGAACCGCCA AAGCGATTTA TGACCGTCCG CAAAGCAGTC ATAGGGGCAA
------------------------------------------------------------------------------
   +2 L  Q  G  G  F  V  W  D  W  V  D  Q  S  L  I  K  Y
      ------------------------------------------------
3051  TACAGGGCGG CTTCGTCTGG GACTGGGTGG ATCAGTCGCT GATTAAATAT
      ATGTCCCGCC GAAGCAGACC CTGACCCACC TAGTCAGCGA CTAATTTATA
------------------------------------------------------------------------------
   +2  D  E  N  G  N  P  W  S  A  Y  G  G  D  F  G  D  T
      ------------------------------------------------
3101  GATGAAAACG GCAACCCGTG GTCGGCTTAC GGCGGTGATT TTGGCGATAC
      CTACTTTTGC CGTTGGGCAC CAGCCGAATG CCGCCACTAA AACCGCTATG
------------------------------------------------------------------------------
   +2  P  N  D  R  Q  F  C  M  N  G  L  V  F  A  D  R
      ------------------------------------------------
3151  GCCGAACGAT CGCCAGTTCT GTATGAACGG TCTGGTCTTT GCCGACCGCA
      CGGCTTGCTA GCGGTCAAGA CATACTTGCC AGACCAGAAA CGGCTGGCGT
------------------------------------------------------------------------------
   +2 T  P  H  P  A  L  T  E  A  K  H  Q  Q  Q  F  F  Q
      ------------------------------------------------
3201  CGCCGCATCC AGCGCTGACG GAAGCAAAAC ACCAGCAGCA GTTTTTCCAG
      GCGGCGTAGG TCGCGACTGC CTTCGTTTTG TGGTCGTCGT CAAAAAGGTC
------------------------------------------------------------------------------
   +2  F  R  L  S  G  Q  T  I  E  V  T  S  E  Y  L  F  R
      ------------------------------------------------
3251  TTCCGTTTAT CCGGGCAAAC CATCGAAGTG ACCAGCGAAT ACCTGTTCCG
      AAGGCAAATA GGCCCGTTTG GTAGCTTCAC TGGTCGCTTA TGGACAAGGC
------------------------------------------------------------------------------
   +2  H  S  D  N  E  L  L  H  W  M  V  A  L  D  G  K
      ------------------------------------------------
3301  TCATAGCGAT AACGAGCTCC TGCACTGGAT GGTGGCGCTG GATGGTAAGC
      AGTATCGCTA TTGCTCGAGG ACGTGACCTA CCACCGCGAC CTACCATTCG
------------------------------------------------------------------------------
   +2 P  L  A  S  G  E  V  P  L  D  V  A  P  Q  G  K  Q
      ------------------------------------------------
3351  CGCTGGCAAG CGGTGAAGTG CCTCTGGATG TCGCTCCACA AGGTAAACAG
      GCGACCGTTC GCCACTTCAC GGAGACCTAC AGCGAGGTGT TCCATTTGTC
------------------------------------------------------------------------------
   +2  L  I  E  L  P  E  L  P  Q  P  E  S  A  G  Q  L  W
      ------------------------------------------------
3401  TTGATTGAAC TGCCTGAACT ACCGCAGCCG GAGAGCGCCG GGCAACTCTG
      AACTAACTTG ACGGACTTGA TGGCGTCGGC CTCTCGCGGC CCGTTGAGAC
------------------------------------------------------------------------------
   +2  L  T  V  R  V  V  Q  P  N  A  T  A  W  S  E  A
      ------------------------------------------------
3451  GCTCACAGTA CGCGTAGTGC AACCGAACGC GACCGCATGG TCAGAAGCCG
      CGAGTGTCAT GCGCATCACG TTGGCTTGCG CTGGCGTACC AGTCTTCGGC
------------------------------------------------------------------------------
```

```
   +2 G  H  I  S  A  W  Q  Q  W  R  L  A  E  N  L  S  V
      ----------------------------------------------------
3501  GGCACATCAG CGCCTGGCAG CAGTGGCGTC TGGCGGAAAA CCTCAGTGTG
      CCGTGTAGTC GCGGACCGTC GTCACCGCAG ACCGCCTTTT GGAGTCACAC
-------------------------------------------------------------------------------
   +2 T  L  P  A  A  S  H  A  I  P  H  L  T  T  S  E  M
      ----------------------------------------------------
3551  ACGCTCCCCG CCGCGTCCCA CGCCATCCCG CATCTGACCA CCAGCGAAAT
      TGCGAGGGGC GGCGCAGGGT GCGGTAGGGC GTAGACTGGT GGTCGCTTTA
-------------------------------------------------------------------------------
   +2  D  F  C  I  E  L  G  N  K  R  W  Q  F  N  R  Q
      ----------------------------------------------------
3601  GGATTTTTGC ATCGAGCTGG GTAATAAGCG TTGGCAATTT AACCGCCAGT
      CCTAAAAACG TAGCTCGACC CATTATTCGC AACCGTTAAA TTGGCGGTCA
-------------------------------------------------------------------------------
   +2 S  G  F  L  S  Q  M  W  I  G  D  K  K  Q  L  L  T
      ----------------------------------------------------
3651  CAGGCTTTCT TTCACAGATG TGGATTGGCG ATAAAAAACA ACTGCTGACG
      GTCCGAAAGA AAGTGTCTAC ACCTAACCGC TATTTTTTGT TGACGACTGC
-------------------------------------------------------------------------------
   +2  P  L  R  D  Q  F  T  R  A  P  L  D  N  D  I  G  V
      ----------------------------------------------------
3701  CCGCTGCGCG ATCAGTTCAC CCGTGCACCG CTGGATAACG ACATTGGCGT
      GGCGACGCGC TAGTCAAGTG GGCACGTGGC GACCTATTGC TGTAACCGCA
-------------------------------------------------------------------------------
   +2  S  E  A  T  R  I  D  P  N  A  W  V  E  R  W  K
      ----------------------------------------------------
3751  AAGTGAAGCG ACCCGCATTG ACCCTAACGC CTGGGTCGAA CGCTGGAAGG
      TTCACTTCGC TGGGCGTAAC TGGGATTGCG GACCCAGCTT GCGACCTTCC
-------------------------------------------------------------------------------
   +2 A  A  G  H  Y  Q  A  E  A  A  L  L  Q  C  T  A  D
      ----------------------------------------------------
3801  CGGCGGGCCA TTACCAGGCC GAAGCAGCGT TGTTGCAGTG CACGGCAGAT
      GCCGCCCGGT AATGGTCCGG CTTCGTCGCA ACAACGTCAC GTGCCGTCTA
-------------------------------------------------------------------------------
   +2  T  L  A  D  A  V  L  I  T  T  A  H  A  W  Q  H  Q
      ----------------------------------------------------
3851  ACACTTGCTG ATGCGGTGCT GATTACGACC GCTCACGCGT GGCAGCATCA
      TGTGAACGAC TACGCCACGA CTAATGCTGG CGAGTGCGCA CCGTCGTAGT
-------------------------------------------------------------------------------
   +2  G  K  T  L  F  I  S  R  K  T  Y  R  I  D  G  S
      ----------------------------------------------------
3901  GGGGAAAACC TTATTTATCA GCCGGAAAAC CTACCGGATT GATGGTAGTG
      CCCCTTTTGG AATAAATAGT CGGCCTTTTG GATGGCCTAA CTACCATCAC
-------------------------------------------------------------------------------
   +2 G  Q  M  A  I  T  V  D  V  E  V  A  S  D  T  P  H
      ----------------------------------------------------
3951  GTCAAATGGC GATTACCGTT GATGTTGAAG TGGCGAGCGA TACACCGCAT
      CAGTTTACCG CTAATGGCAA CTACAACTTC ACCGCTCGCT ATGTGGCGTA
-------------------------------------------------------------------------------
   +2  P  A  R  I  G  L  N  C  Q  L  A  Q  V  A  E  R  V
      ----------------------------------------------------
4001  CCGGCGCGGA TTGGCCTGAA CTGCCAGCTG GCGCAGGTAG CAGAGCGGGT
      GGCCGCGCCT AACCGGACTT GACGGTCGAC CGCGTCCATC GTCTCGCCCA
-------------------------------------------------------------------------------
   +2  N  W  L  G  L  G  P  Q  E  N  Y  P  D  R  L  T
      ----------------------------------------------------
4051  AAACTGGCTC GGATTAGGGC CGCAAGAAAA CTATCCCGAC CGCCTTACTG
      TTTGACCGAG CCTAATCCCG GCGTTCTTTT GATAGGGCTG GCGGAATGAC
-------------------------------------------------------------------------------
```

```
   +2 A  A  C  F  D  R  W  D  L  P  L  S  D  M  Y  T  P
      ---------------------------------------------------
4101  CCGCCTGTTT TGACCGCTGG GATCTGCCAT TGTCAGACAT GTATACCCCG
      GGCGGACAAA ACTGGCGACC CTAGACGGTA ACAGTCTGTA CATATGGGGC
-------------------------------------------------------------------------------

   +2  Y  V  F  P  S  E  N  G  L  R  C  G  T  R  E  L  N
      ---------------------------------------------------
4151  TACGTCTTCC CGAGCGAAAA CGGTCTGCGC TGCGGGACGC GCGAATTGAA
      ATGCAGAAGG GCTCGCTTTT GCCAGACGCG ACGCCCTGCG CGCTTAACTT
-------------------------------------------------------------------------------

   +2    Y  G  P  H  Q  W  R  G  D  F  Q  F  N  I  S  R
      ---------------------------------------------------
4201  TTATGGCCCA CACCAGTGGC GCGGCGACTT CCAGTTCAAC ATCAGCCGCT
      AATACCGGGT GTGGTCACCG CGCCGCTGAA GGTCAAGTTG TAGTCGGCGA
-------------------------------------------------------------------------------

   +2 Y  S  Q  Q  Q  L  M  E  T  S  H  R  H  L  L  H  A
      ---------------------------------------------------
4251  ACAGTCAACA GCAACTGATG GAAACCAGCC ATCGCCATCT GCTGCACGCG
      TGTCAGTTGT CGTTGACTAC CTTTGGTCGG TAGCGGTAGA CGACGTGCGC
-------------------------------------------------------------------------------

   +2  E  E  G  T  W  L  N  I  D  G  F  H  M  G  I  G  G
      ---------------------------------------------------
4301  GAAGAAGGCA CATGGCTGAA TATCGACGGT TTCCATATGG GGATTGGTGG
      CTTCTTCCGT GTACCGACTT ATAGCTGCCA AAGGTATACC CCTAACCACC
-------------------------------------------------------------------------------

   +2   D  D  S  W  S  P  S  V  S  A  E  F  Q  L  S  A
      ---------------------------------------------------
4351  CGACGACTCC TGGAGCCCGT CAGTATCGGC GGAATTCCAG CTGAGCGCCG
      GCTGCTGAGG ACCTCGGGCA GTCATAGCCG CCTTAAGGTC GACTCGCGGC
-------------------------------------------------------------------------------

   +2 G  R  Y  H  Y  Q  L  V  W  C  Q  K  R  S  D  Y  K
      ---------------------------------------------------
4401  GTCGCTACCA TTACCAGTTG GTCTGGTGTC AAAAAAGATC TGACTATAAA
      CAGCGATGGT AATGGTCAAC CAGACCACAG TTTTTTCTAG ACTGATATTT
-------------------------------------------------------------------------------

   +2  D  E  D  L  D  H  H  H  H  H  H  R
      ------------------------------------>
4451  GATGAGGACC TCGACCATCA TCATCATCAT CACCGGTAAT AATAGGTAGA
      CTACTCCTGG AGCTGGTAGT AGTAGTAGTA GTGGCCATTA TTATCCATCT
-------------------------------------------------------------------------------

4501  TAAGTGACTG ATTAGATGCA TTGATCCCTC GACCAATTCC GGTTATTTTC
      ATTCACTGAC TAATCTACGT AACTAGGGAG CTGGTTAAGG CCAATAAAAG
-------------------------------------------------------------------------------

4551  CACCATATTG CCGTCTTTTG GCAATGTGAG GGCCCGGAAA CCTGGCCCTG
      GTGGTATAAC GGCAGAAAAC CGTTACACTC CCGGGCCTTT GGACCGGGAC
-------------------------------------------------------------------------------

4601  TCTTCTTGAC GAGCATTCCT AGGGGTCTTT CCCCTCTCGC CAAAGGAATG
      AGAAGAACTG CTCGTAAGGA TCCCCAGAAA GGGGAGAGCG GTTTCCTTAC
-------------------------------------------------------------------------------

4651  CAAGGTCTGT TGAATGTCGT GAAGGAAGCA GTTCCTCTGG AAGCTTCTTG
      GTTCCAGACA ACTTACAGCA CTTCCTTCGT CAAGGAGACC TTCGAAGAAC
-------------------------------------------------------------------------------

4701  AAGACAAACA ACGTCTGTAG CGACCCTTTG CAGGCAGCGG AACCCCCCAC
      TTCTGTTTGT TGCAGACATC GCTGGGAAAC GTCCGTCGCC TTGGGGGGTG
-------------------------------------------------------------------------------

4751  CTGGCGACAG GTGCCTCTGC GGCCAAAAGC CACGTGTATA AGATACACCT
      GACCGCTGTC CACGGAGACG CCGGTTTTCG GTGCACATAT TCTATGTGGA
-------------------------------------------------------------------------------
```

```
4801  GCAAAGGCGG CACAACCCCA GTGCCACGTT GTGAGTTGGA TAGTTGTGGA
      CGTTTCCGCC GTGTTGGGGT CACGGTGCAA CACTCAACCT ATCAACACCT
-------------------------------------------------------------------------------
4851  AAGAGTCAAA TGGCTCTCCT CAAGCGTATT CAACAAGGGG CTGAAGGATG
      TTCTCAGTTT ACCGAGAGGA GTTCGCATAA GTTGTTCCCC GACTTCCTAC
-------------------------------------------------------------------------------
4901  CCCAGAAGGT ACCCCATTGT ATGGGATCTG ATCTGGGGCC TCGGTGCACA
      GGGTCTTCCA TGGGGTAACA TACCCTAGAC TAGACCCCGG AGCCACGTGT
-------------------------------------------------------------------------------
4951  TGCTTTACAT GTGTTTAGTC GAGGTTAAAA AACGTCTAGG CCCCCCGAAC
      ACGAAATGTA CACAAATCAG CTCCAATTTT TTGCAGATCC GGGGGGCTTG
-------------------------------------------------------------------------------
5001  CACGGGGACG TGGTTTTCCT TTGAAAAACA CGATGATAAT ACCATGATTG
      GTGCCCCTGC ACCAAAAGGA AACTTTTTGT GCTACTATTA TGGTACTAAC
-------------------------------------------------------------------------------
5051  AACAAGATGG ATTGCACGCA GGTTCTCCGG CCGCTTGGGT GGAGAGGCTA
      TTGTTCTACC TAACGTGCGT CCAAGAGGCC GGCGAACCCA CCTCTCCGAT
-------------------------------------------------------------------------------
5101  TTCGGCTATG ACTGGGCACA ACAGACAATC GGCTGCTCTG ATGCCGCCGT
      AAGCCGATAC TGACCCGTGT TGTCTGTTAG CCGACGAGAC TACGGCGGCA
-------------------------------------------------------------------------------
5151  GTTCCGGCTG TCAGCGCAGG GGCGCCCGGT TCTTTTTGTC AAGACCGACC
      CAAGGCCGAC AGTCGCGTCC CCGCGGGCCA AGAAAAACAG TTCTGGCTGG
-------------------------------------------------------------------------------
5201  TGTCCGGTGC CCTGAATGAA CTGCAGGACG AGGCAGCGCG GCTATCGTGG
      ACAGGCCACG GGACTTACTT GACGTCCTGC TCCGTCGCGC CGATAGCACC
-------------------------------------------------------------------------------
5251  CTGGCCACGA CGGGCGTTCC TTGCGCAGCT GTGCTCGACG TTGTCACTGA
      GACCGGTGCT GCCCGCAAGG AACGCGTCGA CACGAGCTGC AACAGTGACT
-------------------------------------------------------------------------------
5301  AGCGGGAAGG GACTGGCTGC TATTGGGCGA AGTGCCGGGG CAGGATCTCC
      TCGCCCTTCC CTGACCGACG ATAACCCGCT TCACGGCCCC GTCCTAGAGG
-------------------------------------------------------------------------------
5351  TGTCATCTCA CCTTGCTCCT GCCGAGAAAG TATCCATCAT GGCTGATGCA
      ACAGTAGAGT GGAACGAGGA CGGCTCTTTC ATAGGTAGTA CCGACTACGT
-------------------------------------------------------------------------------
5401  ATGCGGCGGC TGCATACGCT TGATCCGGCT ACCTGCCCAT TCGACCACCA
      TACGCCGCCG ACGTATGCGA ACTAGGCCGA TGGACGGGTA AGCTGGTGGT
-------------------------------------------------------------------------------
5451  AGCGAAACAT CGCATCGAGC GAGCACGTAC TCGGATGGAA GCCGGTCTTG
      TCGCTTTGTA GCGTAGCTCG CTCGTGCATG AGCCTACCTT CGGCCAGAAC
-------------------------------------------------------------------------------
5501  TCGATCAGGA TGATCTGGAC GAAGAGCATC AGGGGCTCGC GCCAGCCGAA
      AGCTAGTCCT ACTAGACCTG CTTCTCGTAG TCCCCGAGCG CGGTCGGCTT
-------------------------------------------------------------------------------
5551  CTGTTCGCCA GGCTCAAGGC GCGCATGCCC GACGGCGAGG ATCTCGTCGT
      GACAAGCGGT CCGAGTTCCG CGCGTACGGG CTGCCGCTCC TAGAGCAGCA
-------------------------------------------------------------------------------
5601  GACCCATGGC GATGCCTGCT TGCCGAATAT CATGGTGGAA AATGGCCGCT
      CTGGGTACCG CTACGGACGA ACGGCTTATA GTACCACCTT TTACCGGCGA
-------------------------------------------------------------------------------
5651  TTTCTGGATT CATCGACTGT GGCCGGCTGG GTGTGGCGGA CCGCTATCAG
      AAAGACCTAA GTAGCTGACA CCGGCCGACC CACACCGCCT GGCGATAGTC
-------------------------------------------------------------------------------
5701  GACATAGCGT TGGCTACCCG TGATATTGCT GAAGAGCTTG GCGGCGAATG
      CTGTATCGCA ACCGATGGGC ACTATAACGA CTTCTCGAAC CGCCGCTTAC
-------------------------------------------------------------------------------
```

```
5751  GGCTGACCGC TTCCTCGTGC TTTACGGTAT CGCCGCTCCC GATTCGCAGC
      CCGACTGGCG AAGGAGCACG AAATGCCATA GCGGCGAGGG CTAAGCGTCG
-------------------------------------------------------------------------------
5801  GCATCGCCTT CTATCGCCTT CTTGACGAGT TCTTCTGAGC GGGACTCTGG
      CGTAGCGGAA GATAGCGGAA GAACTGCTCA AGAAGACTCG CCCTGAGACC
-------------------------------------------------------------------------------
5851  GGTTCGCATC GATAAAATAA AAGATTTTAT TTAGTCTCCA GAAAAAGGGG
      CCAAGCGTAG CTATTTTATT TTCTAAAATA AATCAGAGGT CTTTTTCCCC
-------------------------------------------------------------------------------
5901  GGAATGAAAG ACCCCACCTG TAGGTTTGGC AAGCTAGCTT AAGTAACGCC
      CCTTACTTTC TGGGGTGGAC ATCCAAACCG TTCGATCGAA TTCATTGCGG
-------------------------------------------------------------------------------
5951  ATTTTGCAAG GCATGGAAAA ATACATAACT GAGAATAGAG AAGTTCAGAT
      TAAAACGTTC CGTACCTTTT TATGTATTGA CTCTTATCTC TTCAAGTCTA
-------------------------------------------------------------------------------
6001  CAAGGTCAGG AACAGATGGA ACAGCTGAAT ATGGGCCAAA CAGGATATCT
      GTTCCAGTCC TTGTCTACCT TGTCGACTTA TACCCGGTTT GTCCTATAGA
-------------------------------------------------------------------------------
6051  GTGGTAAGCA GTTCCTGCCC CGGCTCAGGG CCAAGAACAG ATGGAACAGC
      CACCATTCGT CAAGGACGGG GCCGAGTCCC GGTTCTTGTC TACCTTGTCG
-------------------------------------------------------------------------------
6101  TGAATATGGG CCAAACAGGA TATCTGTGGT AAGCAGTTCC TGCCCCGGCT
      ACTTATACCC GGTTTGTCCT ATAGACACCA TTCGTCAAGG ACGGGGCCGA
-------------------------------------------------------------------------------
6151  CAGGGCCAAG AACAGATGGT CCCCAGATGC GGTCCAGCCC TCAGCAGTTT
      GTCCCGGTTC TTGTCTACCA GGGGTCTACG CCAGGTCGGG AGTCGTCAAA
-------------------------------------------------------------------------------
6201  CTAGAGAACC ATCAGATGTT TCCAGGGTGC CCCAAGGACC TGAAATGACC
      GATCTCTTGG TAGTCTACAA AGGTCCCACG GGGTTCCTGG ACTTTACTGG
-------------------------------------------------------------------------------
6251  CTGTGCCTTA TTTGAACTAA CCAATCAGTT CGCTTCTCGC TTCTGTTCGC
      GACACGGAAT AAACTTGATT GGTTAGTCAA GCGAAGAGCG AAGACAAGCG
-------------------------------------------------------------------------------
6301  GCGCTTCTGC TCCCCGAGCT CAATAAAAGA GCCCACAACC CCTCACTCGG
      CGCGAAGACG AGGGGCTCGA GTTATTTTCT CGGGTGTTGG GGAGTGAGCC
-------------------------------------------------------------------------------
6351  GGCGCCAGTC CTCCGATTGA CTGAGTCGCC CGGGTACCCG TGTATCCAAT
      CCGCGGTCAG GAGGCTAACT GACTCAGCGG GCCCATGGGC ACATAGGTTA
-------------------------------------------------------------------------------
6401  AAACCCTCTT GCAGTTGCAT CCGACTTGTG GTCTCGCTGT TCCTTGGGAG
      TTTGGGAGAA CGTCAACGTA GGCTGAACAC CAGAGCGACA AGGAACCCTC
-------------------------------------------------------------------------------
6451  GGTCTCCTCT GAGTGATTGA CTACCCGTCA GCGGGGGTCT TTCATTCATG
      CCAGAGGAGA CTCACTAACT GATGGGCAGT CGCCCCCAGA AAGTAAGTAC
-------------------------------------------------------------------------------
6501  CAGCATGTAT CAAAATTAAT TTGGTTTTTT TTCTTAAGTA TTTACATTAA
      GTCGTACATA GTTTTAATTA AACCAAAAAA AAGAATTCAT AAATGTAATT
-------------------------------------------------------------------------------
6551  ATGGCCATAG TTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT
      TACCGGTATC AACGTAATTA CTTAGCCGGT TGCGCGCCCC TCTCCGCCAA
-------------------------------------------------------------------------------
6601  TGCGTATTGG CGCTCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG
      ACGCATAACC GCGAGAAGGC GAAGGAGCGA GTGACTGAGC GACGCGAGCC
-------------------------------------------------------------------------------
6651  TCGTTCGGCT GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG
      AGCAAGCCGA CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC
-------------------------------------------------------------------------------
```

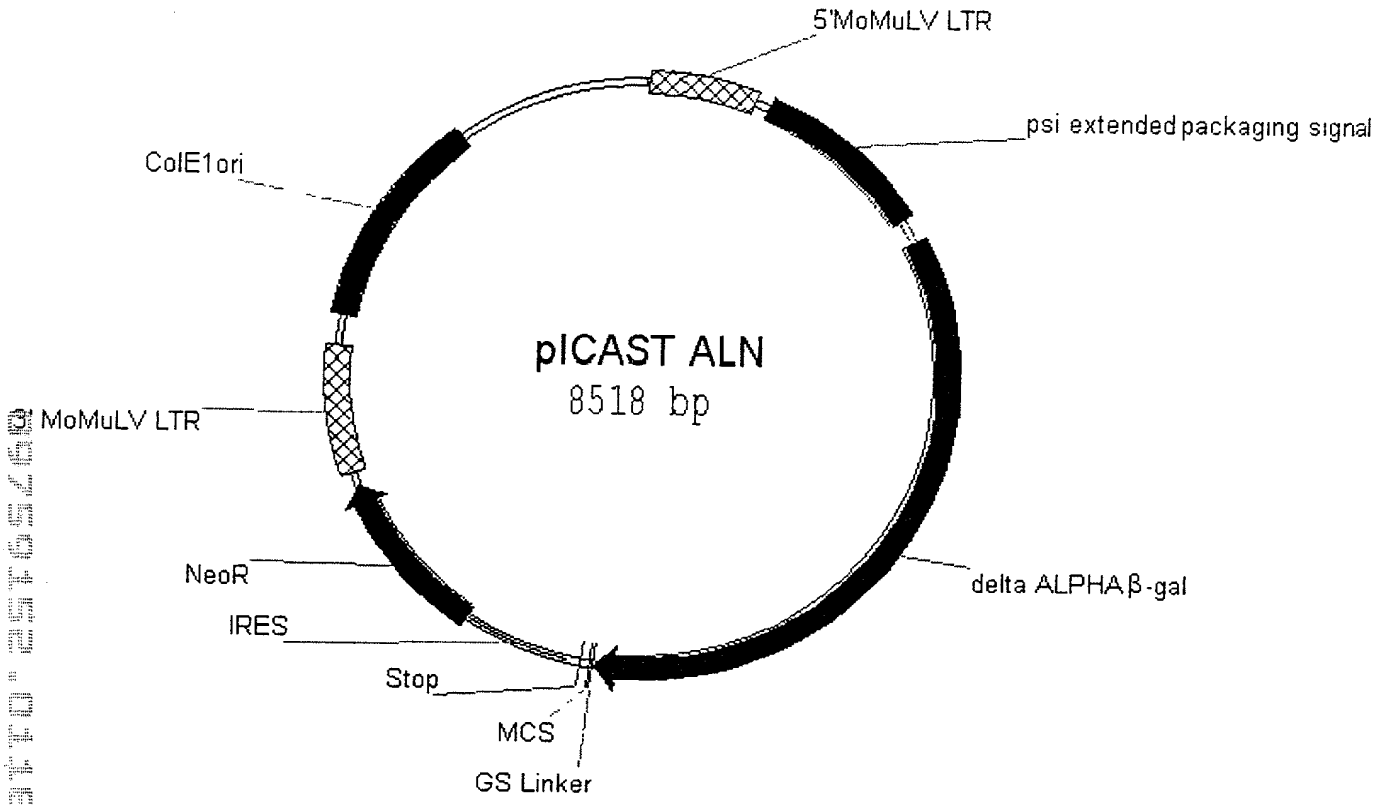
5'MoMuLV LTR
psi extended packaging signal
ColE1ori
pICAST ALN
8518 bp
3' MoMuLV LTR
NeoR
IRES
Stop
MCS
GS Linker
delta ALPHA β-gal

Figure 11A

```
  1  CTGCAGCCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG
     GACGTCGGAC TTATACCCGG TTTGTCCTAT AGACACCATT CGTCAAGGAC
---------------------------------------------------------------------------
 51  CCCCGGCTCA GGGCCAAGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA
     GGGGCCGAGT CCCGGTTCTT GTCTACCTTG TCGACTTATA CCCGGTTTGT
---------------------------------------------------------------------------
101  GGATATCTGT GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT
     CCTATAGACA CCATTCGTCA AGGACGGGGC CGAGTCCCGG TTCTTGTCTA
---------------------------------------------------------------------------
151  GGTCCCCAGA TGCGGTCCAG CCCTCAGCAG TTTCTAGAGA ACCATCAGAT
     CCAGGGGTCT ACGCCAGGTC GGGAGTCGTC AAAGATCTCT TGGTAGTCTA
---------------------------------------------------------------------------
201  GTTTCCAGGG TGCCCCAAGG ACCTGAAATG ACCCTGTGCC TTATTTGAAC
     CAAAGGTCCC ACGGGGTTCC TGGACTTTAC TGGGACACGG AATAAACTTG
---------------------------------------------------------------------------
251  TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC TGCTCCCCGA
     ATTGGTTAGT CAAGCGAAGA GCGAAGACAA GCGCGCGAAG ACGAGGGGCT
---------------------------------------------------------------------------
301  GCTCAATAAA AGAGCCCACA ACCCCTCACT CGGGGCGCCA GTCCTCCGAT
     CGAGTTATTT TCTCGGGTGT TGGGGAGTGA GCCCCGCGGT CAGGAGGCTA
---------------------------------------------------------------------------
351  TGACTGAGTC GCCCGGGTAC CCGTGTATCC AATAAACCCT CTTGCAGTTG
     ACTGACTCAG CGGGCCCATG GCACATAGG TTATTTGGGA GAACGTCAAC
---------------------------------------------------------------------------
401  CATCCGACTT GTGGTCTCGC TGTTCCTTGG GAGGGTCTCC TCTGAGTGAT
     GTAGGCTGAA CACCAGAGCG ACAAGGAACC CTCCCAGAGG AGACTCACTA
---------------------------------------------------------------------------
451  TGACTACCCG TCAGCGGGGG TCTTTCATTT GGGGGCTCGT CCGGGATCGG
     ACTGATGGGC AGTCGCCCCC AGAAAGTAAA CCCCCGAGCA GGCCCTAGCC
---------------------------------------------------------------------------
501  GAGACCCCTG CCCAGGGACC ACCGACCCAC CACCGGGAGG CAAGCTGGCC
     CTCTGGGGAC GGGTCCCTGG TGGCTGGGTG GTGGCCCTCC GTTCGACCGG
---------------------------------------------------------------------------
551  AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG ACTGATTTTA
     TCGTTGAATA GACACAGACA GGCTAACAGA TCACAGATAC TGACTAAAAT
---------------------------------------------------------------------------
601  TGCGCCTGCG TCGGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC
     ACGCGGACGC AGCCATGATC AATCGATTGA TCGAGACATA GACCGCCTGG
---------------------------------------------------------------------------
651  CGTGGTGGAA CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG
     GCACCACCTT GACTGCTCAA GACTTGTGGG CCGGCGTTGG GACCCTCTGC
---------------------------------------------------------------------------
701  TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG CCCGACCTGA GGAAGGGAGT
     AGGGTCCCTG AAACCCCCGG CAAAAACACC GGGCTGGACT CCTTCCCTCA
---------------------------------------------------------------------------
751  CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT AGGAGACGAG
     GCTACACCTT AGGCTGGGGC AGTCCTATAC ACCAAGACCA TCCTCTGCTC
---------------------------------------------------------------------------
801  AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA
     TTGGATTTTG TCAAGGGCGG AGGCAGACTT AAAAACGAAA GCCAAACCTT
---------------------------------------------------------------------------
851  CCGAAGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT
     GGCTTCGGCG CGCAGAACAG ACGACGTCGT AGCAAGACAC AACAGAGACA
---------------------------------------------------------------------------
901  CTGACTGTGT TTCTGTATTT GTCTGAAAAT TAGGGCCAGA CTGTTACCAC
     GACTGACACA AAGACATAAA CAGACTTTTA ATCCCGGTCT GACAATGGTG
---------------------------------------------------------------------------
```

FIGURE 11B

```
 951  TCCCTTAAGT TTGACCTTAG GTAACTGGAA AGATGTCGAG CGGCTCGCTC
      AGGGAATTCA AACTGGAATC CATTGACCTT TCTACAGCTC GCCGAGCGAG
------------------------------------------------------------------------------
1001  ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
      TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
------------------------------------------------------------------------------
1051  GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
      CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
------------------------------------------------------------------------------
1101  CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
      GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
------------------------------------------------------------------------------
1151  ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
      TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
------------------------------------------------------------------------------
1201  TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
      AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
------------------------------------------------------------------------------
1251  TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
      AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
------------------------------------------------------------------------------
1301  CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
      GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
------------------------------------------------------------------------------
1351  GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAACACCA
      CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTGTGGT
------------------------------------------------------------------------------
1401  TGCACCATCA TCATCATCAC GTCGACTATA AAGATGAGGA CCTCGAGATG
      ACGTGGTAGT AGTAGTAGTG CAGCTGATAT TTCTACTCCT GGAGCTCTAC
------------------------------------------------------------------------------
1451  GGCGTGATTA CGGATTCACT GGCCGTCGTG GCCCGCACCG ATCGCCCTTC
      CCGCACTAAT GCCTAAGTGA CCGGCAGCAC CGGGCGTGGC TAGCGGGAAG
------------------------------------------------------------------------------
1501  CCAACAGTTA CGCAGCCTGA ATGGCGAATG GCGCTTTGCC TGGTTTCCGG
      GGTTGTCAAT GCGTCGGACT TACCGCTTAC CGCGAAACGG ACCAAAGGCC
------------------------------------------------------------------------------
1551  CACCAGAAGC GGTGCCGGAA AGCTGGCTGG AGTGCGATCT TCCTGAGGCC
      GTGGTCTTCG CCACGGCCTT TCGACCGACC TCACGCTAGA AGGACTCCGG
------------------------------------------------------------------------------
1601  GATACTGTCG TCGTCCCCTC AAACTGGCAG ATGCACGGTT ACGATGCGCC
      CTATGACAGC AGCAGGGGAG TTTGACCGTC TACGTGCCAA TGCTACGCGG
------------------------------------------------------------------------------
1651  CATCTACACC AACGTGACCT ATCCCATTAC GGTCAATCCG CCGTTTGTTC
      GTAGATGTGG TTGCACTGGA TAGGGTAATG CCAGTTAGGC GGCAAACAAG
------------------------------------------------------------------------------
1701  CCACGGAGAA TCCGACGGGT TGTTACTCGC TCACATTTAA TGTTGATGAA
      GGTGCCTCTT AGGCTGCCCA ACAATGAGCG AGTGTAAATT ACAACTACTT
------------------------------------------------------------------------------
1751  AGCTGGCTAC AGGAAGGCCA GACGCGAATT ATTTTTGATG GCGTTAACTC
      TCGACCGATG TCCTTCCGGT CTGCGCTTAA TAAAAACTAC CGCAATTGAG
------------------------------------------------------------------------------
1801  GGCGTTTCAT CTGTGGTGCA ACGGGCGCTG GGTCGGTTAC GGCCAGGACA
      CCGCAAAGTA GACACCACGT TGCCCGCGAC CCAGCCAATG CCGGTCCTGT
------------------------------------------------------------------------------
1851  GTCGTTTGCC GTCTGAATTT GACCTGAGCG CATTTTTACG CGCCGGAGAA
      CAGCAAACGG CAGACTTAAA CTGGACTCGC GTAAAAATGC GCGGCCTCTT
------------------------------------------------------------------------------
```

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1901  AACCGCCTCG CGGTGATGGT GCTGCGCTGG AGTGACGGCA GTTATCTGGA
      TTGGCGGAGC GCCACTACCA CGACGCGACC TCACTGCCGT CAATAGACCT
-------------------------------------------------------------------------------
1951  AGATCAGGAT ATGTGGCGGA TGAGCGGCAT TTTCCGTGAC GTCTCGTTGC
      TCTAGTCCTA TACACCGCCT ACTCGCCGTA AAAGGCACTG CAGAGCAACG
-------------------------------------------------------------------------------
2001  TGCATAAACC GACTACACAA ATCAGCGATT TCCATGTTGC CACTCGCTTT
      ACGTATTTGG CTGATGTGTT TAGTCGCTAA AGGTACAACG GTGAGCGAAA
-------------------------------------------------------------------------------
2051  AATGATGATT TCAGCCGCGC TGTACTGGAG GCTGAAGTTC AGATGTGCGG
      TTACTACTAA AGTCGGCGCG ACATGACCTC CGACTTCAAG TCTACACGCC
-------------------------------------------------------------------------------
2101  CGAGTTGCGT GACTACCTAC GGGTAACAGT TTCTTTATGG CAGGGTGAAA
      GCTCAACGCA CTGATGGATG CCCATTGTCA AAGAAATACC GTCCCACTTT
-------------------------------------------------------------------------------
2151  CGCAGGTCGC CAGCGGCACC GCGCCTTTCG GCGGTGAAAT TATCGATGAG
      GCGTCCAGCG GTCGCCGTGG CGCGGAAAGC CGCCACTTTA ATAGCTACTC
-------------------------------------------------------------------------------
2201  CGTGGTGGTT ATGCCGATCG CGTCACACTA CGTCTGAACG TCGAAAACCC
      GCACCACCAA TACGGCTAGC GCAGTGTGAT GCAGACTTGC AGCTTTTGGG
-------------------------------------------------------------------------------
2251  GAAACTGTGG AGCGCCGAAA TCCCGAATCT CTATCGTGCG GTGGTTGAAC
      CTTTGACACC TCGCGGCTTT AGGGCTTAGA GATAGCACGC CACCAACTTG
-------------------------------------------------------------------------------
2301  TGCACACCGC CGACGGCACG CTGATTGAAG CAGAAGCCTG CGATGTCGGT
      ACGTGTGGCG GCTGCCGTGC GACTAACTTC GTCTTCGGAC GCTACAGCCA
-------------------------------------------------------------------------------
2351  TTCCGCGAGG TGCGGATTGA AAATGGTCTG CTGCTGCTGA ACGGCAAGCC
      AAGGCGCTCC ACGCCTAACT TTTACCAGAC GACGACGACT TGCCGTTCGG
-------------------------------------------------------------------------------
2401  GTTGCTGATT CGAGGCGTTA ACCGTCACGA GCATCATCCT CTGCATGGTC
      CAACGACTAA GCTCCGCAAT TGGCAGTGCT CGTAGTAGGA GACGTACCAG
-------------------------------------------------------------------------------
2451  AGGTCATGGA TGAGCAGACG ATGGTGCAGG ATATCCTGCT GATGAAGCAG
      TCCAGTACCT ACTCGTCTGC TACCACGTCC TATAGGACGA CTACTTCGTC
-------------------------------------------------------------------------------
2501  AACAACTTTA ACGCCGTGCG CTGTTCGCAT TATCCGAACC ATCCGCTGTG
      TTGTTGAAAT TGCGGCACGC GACAAGCGTA ATAGGCTTGG TAGGCGACAC
-------------------------------------------------------------------------------
2551  GTACACGCTG TGCGACCGCT ACGGCCTGTA TGTGGTGGAT GAAGCCAATA
      CATGTGCGAC ACGCTGGCGA TGCCGGACAT ACACCACCTA CTTCGGTTAT
-------------------------------------------------------------------------------
2601  TTGAAACCCA CGGCATGGTG CCAATGAATC GTCTGACCGA TGATCCGCGC
      AACTTTGGGT GCCGTACCAC GGTTACTTAG CAGACTGGCT ACTAGGCGCG
-------------------------------------------------------------------------------
2651  TGGCTACCGG CGATGAGCGA ACGCGTAACG CGAATGGTGC AGCGCGATCG
      ACCGATGGCC GCTACTCGCT TGCGCATTGC GCTTACCACG TCGCGCTAGC
-------------------------------------------------------------------------------
2701  TAATCACCCG AGTGTGATCA TCTGGTCGCT GGGGAATGAA TCAGGCCACG
      ATTAGTGGGC TCACACTAGT AGACCAGCGA CCCCTTACTT AGTCCGGTGC
-------------------------------------------------------------------------------
2751  GCGCTAATCA CGACGCGCTG TATCGCTGGA TCAAATCTGT CGATCCTTCC
      CGCGATTAGT GCTGCGCGAC ATAGCGACCT AGTTTAGACA GCTAGGAAGG
-------------------------------------------------------------------------------
2801  CGCCCGGTGC AGTATGAAGG CGGCGGAGCC GACACCACGG CCACCGATAT
      GCGGGCCACG TCATACTTCC GCCGCCTCGG CTGTGGTGCC GGTGGCTATA
-------------------------------------------------------------------------------
```

```
2851  TATTTGCCCG ATGTACGCGC GCGTGGATGA AGACCAGCCC TTCCCGGCTG
      ATAAACGGGC TACATGCGCG CGCACCTACT TCTGGTCGGG AAGGGCCGAC
-------------------------------------------------------------------------------
2901  TGCCGAAATG GTCCATCAAA AAATGGCTTT CGCTACCTGG AGAGACGCGC
      ACGGCTTTAC CAGGTAGTTT TTTACCGAAA GCGATGGACC TCTCTGCGCG
-------------------------------------------------------------------------------
2951  CCGCTGATCC TTTGCGAATA CGCCCACGCG ATGGGTAACA GTCTTGGCGG
      GGCGACTAGG AAACGCTTAT GCGGGTGCGC TACCCATTGT CAGAACCGCC
-------------------------------------------------------------------------------
3001  TTTCGCTAAA TACTGGCAGG CGTTTCGTCA GTATCCCCGT TTACAGGGCG
      AAAGCGATTT ATGACCGTCC GCAAAGCAGT CATAGGGGCA AATGTCCCGC
-------------------------------------------------------------------------------
3051  GCTTCGTCTG GGACTGGGTG GATCAGTCGC TGATTAAATA TGATGAAAAC
      CGAAGCAGAC CCTGACCCAC CTAGTCAGCG ACTAATTTAT ACTACTTTTG
-------------------------------------------------------------------------------
3101  GGCAACCCGT GGTCGGCTTA CGGCGGTGAT TTTGGCGATA CGCCGAACGA
      CCGTTGGGCA CCAGCCGAAT GCCGCCACTA AAACCGCTAT GCGGCTTGCT
-------------------------------------------------------------------------------
3151  TCGCCAGTTC TGTATGAACG GTCTGGTCTT TGCCGACCGC ACGCCGCATC
      AGCGGTCAAG ACATACTTGC CAGACCAGAA ACGGCTGGCG TGCGGCGTAG
-------------------------------------------------------------------------------
3201  CAGCGCTGAC GGAAGCAAAA CACCAGCAGC AGTTTTTCCA GTTCCGTTTA
      GTCGCGACTG CCTTCGTTTT GTGGTCGTCG TCAAAAAGGT CAAGGCAAAT
-------------------------------------------------------------------------------
3251  TCCGGGCAAA CCATCGAAGT GACCAGCGAA TACCTGTTCC GTCATAGCGA
      AGGCCCGTTT GGTAGCTTCA CTGGTCGCTT ATGGACAAGG CAGTATCGCT
-------------------------------------------------------------------------------
3301  TAACGAGCTC CTGCACTGGA TGGTGGCGCT GGATGGTAAG CCGCTGGCAA
      ATTGCTCGAG GACGTGACCT ACCACCGCGA CCTACCATTC GGCGACCGTT
-------------------------------------------------------------------------------
3351  GCGGTGAAGT GCCTCTGGAT GTCGCTCCAC AAGGTAAACA GTTGATTGAA
      CGCCACTTCA CGGAGACCTA CAGCGAGGTG TTCCATTTGT CAACTAACTT
-------------------------------------------------------------------------------
3401  CTGCCTGAAC TACCGCAGCC GGAGAGCGCC GGGCAACTCT GGCTCACAGT
      GACGGACTTG ATGGCGTCGG CCTCTCGCGG CCCGTTGAGA CCGAGTGTCA
-------------------------------------------------------------------------------
3451  ACGCGTAGTG CAACCGAACG CGACCGCATG GTCAGAAGCC GGGCACATCA
      TGCGCATCAC GTTGGCTTGC GCTGGCGTAC CAGTCTTCGG CCCGTGTAGT
-------------------------------------------------------------------------------
3501  GCGCCTGGCA GCAGTGGCGT CTGGCGGAAA ACCTCAGTGT GACGCTCCCC
      CGCGGACCGT CGTCACCGCA GACCGCCTTT TGGAGTCACA CTGCGAGGGG
-------------------------------------------------------------------------------
3551  GCCGCGTCCC ACGCCATCCC GCATCTGACC ACCAGCGAAA TGGATTTTTG
      CGGCGCAGGG TGCGGTAGGG CGTAGACTGG TGGTCGCTTT ACCTAAAAAC
-------------------------------------------------------------------------------
3601  CATCGAGCTG GGTAATAAGC GTTGGCAATT TAACCGCCAG TCAGGCTTTC
      GTAGCTCGAC CCATTATTCG CAACCGTTAA ATTGGCGGTC AGTCCGAAAG
-------------------------------------------------------------------------------
3651  TTTCACAGAT GTGGATTGGC GATAAAAAAC AACTGCTGAC GCCGCTGCGC
      AAAGTGTCTA CACCTAACCG CTATTTTTTG TTGACGACTG CGGCGACGCG
-------------------------------------------------------------------------------
3701  GATCAGTTCA CCCGTGCACC GCTGGATAAC GACATTGGCG TAAGTGAAGC
      CTAGTCAAGT GGGCACGTGG CGACCTATTG CTGTAACCGC ATTCACTTCG
-------------------------------------------------------------------------------
3751  GACCCGCATT GACCCTAACG CCTGGGTCGA ACGCTGGAAG GCGGCGGGCC
      CTGGGCGTAA CTGGGATTGC GGACCCAGCT TGCGACCTTC CGCCGCCCGG
-------------------------------------------------------------------------------
```

```
3801  ATTACCAGGC CGAAGCAGCG TTGTTGCAGT GCACGGCAGA TACACTTGCT
      TAATGGTCCG GCTTCGTCGC AACAACGTCA CGTGCCGTCT ATGTGAACGA
-------------------------------------------------------------------------------
3851  GATGCGGTGC TGATTACGAC CGCTCACGCG TGGCAGCATC AGGGGAAAAC
      CTACGCCACG ACTAATGCTG GCGAGTGCGC ACCGTCGTAG TCCCCTTTTG
-------------------------------------------------------------------------------
3901  CTTATTTATC AGCCGGAAAA CCTACCGGAT TGATGGTAGT GGTCAAATGG
      GAATAAATAG TCGGCCTTTT GGATGGCCTA ACTACCATCA CCAGTTTACC
-------------------------------------------------------------------------------
3951  CGATTACCGT TGATGTTGAA GTGGCGAGCG ATACACCGCA TCCGGCGCGG
      GCTAATGGCA ACTACAACTT CACCGCTCGC TATGTGGCGT AGGCCGCGCC
-------------------------------------------------------------------------------
4001  ATTGGCCTGA ACTGCCAGCT GGCGCAGGTA GCAGAGCGGG TAAACTGGCT
      TAACCGGACT TGACGGTCGA CCGCGTCCAT CGTCTCGCCC ATTTGACCGA
-------------------------------------------------------------------------------
4051  CGGATTAGGG CCGCAAGAAA ACTATCCCGA CCGCCTTACT GCCGCCTGTT
      GCCTAATCCC GGCGTTCTTT TGATAGGGCT GGCGGAATGA CGGCGGACAA
-------------------------------------------------------------------------------
4101  TTGACCGCTG GGATCTGCCA TTGTCAGACA TGTATACCCC GTACGTCTTC
      AACTGGCGAC CCTAGACGGT AACAGTCTGT ACATATGGGG CATGCAGAAG
-------------------------------------------------------------------------------
4151  CCGAGCGAAA ACGGTCTGCG CTGCGGGACG CGCGAATTGA ATTATGGCCC
      GGCTCGCTTT TGCCAGACGC GACGCCCTGC GCGCTTAACT TAATACCGGG
-------------------------------------------------------------------------------
4201  ACACCAGTGG CGCGGCGACT TCCAGTTCAA CATCAGCCGC TACAGTCAAC
      TGTGGTCACC GCGCCGCTGA AGGTCAAGTT GTAGTCGGCG ATGTCAGTTG
-------------------------------------------------------------------------------
4251  AGCAACTGAT GGAAACCAGC CATCGCCATC TGCTGCACGC GGAAGAAGGC
      TCGTTGACTA CCTTTGGTCG GTAGCGGTAG ACGACGTGCG CCTTCTTCCG
-------------------------------------------------------------------------------
4301  ACATGGCTGA ATATCGACGG TTTCCATATG GGGATTGGTG GCGACGACTC
      TGTACCGACT TATAGCTGCC AAAGGTATAC CCCTAACCAC CGCTGCTGAG
-------------------------------------------------------------------------------
4351  CTGGAGCCCG TCAGTATCGG CGGAATTCCA GCTGAGCGCC GGTCGCTACC
      GACCTCGGGC AGTCATAGCC GCCTTAAGGT CGACTCGCGG CCAGCGATGG
-------------------------------------------------------------------------------
4401  ATTACCAGTT GGTCTGGTGT CAAAAAAGAT CTGGAGGTGG TGGCAGCAGG
      TAATGGTCAA CCAGACCACA GTTTTTTCTA GACCTCCACC ACCGTCGTCC
-------------------------------------------------------------------------------
4451  CCTTGGCGCG CCGGATCCTT AATTAACAAT TGACCGGTAA TAATAGGTAG
      GGAACCGCGC GGCCTAGGAA TTAATTGTTA ACTGGCCATT ATTATCCATC
-------------------------------------------------------------------------------
4501  ATAAGTGACT GATTAGATGC ATTGATCCCT CGACCAATTC CGGTTATTTT
      TATTCACTGA CTAATCTACG TAACTAGGGA GCTGGTTAAG GCCAATAAAA
-------------------------------------------------------------------------------
4551  CCACCATATT GCCGTCTTTT GGCAATGTGA GGGCCCGGAA ACCTGGCCCT
      GGTGGTATAA CGGCAGAAAA CCGTTACACT CCCGGGCCTT TGGACCGGGA
-------------------------------------------------------------------------------
4601  GTCTTCTTGA CGAGCATTCC TAGGGGTCTT TCCCCTCTCG CCAAAGGAAT
      CAGAAGAACT GCTCGTAAGG ATCCCCAGAA AGGGGAGAGC GGTTTCCTTA
-------------------------------------------------------------------------------
4651  GCAAGGTCTG TTGAATGTCG TGAAGGAAGC AGTTCCTCTG GAAGCTTCTT
      CGTTCCAGAC AACTTACAGC ACTTCCTTCG TCAAGGAGAC CTTCGAAGAA
-------------------------------------------------------------------------------
4701  GAAGACAAAC AACGTCTGTA GCGACCCTTT GCAGGCAGCG GAACCCCCCA
      CTTCTGTTTG TTGCAGACAT CGCTGGGAAA CGTCCGTCGC CTTGGGGGGT
-------------------------------------------------------------------------------
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4751  CCTGGCGACA GGTGCCTCTG CGGCCAAAAG CCACGTGTAT AAGATACACC
      GGACCGCTGT CCACGGAGAC GCCGGTTTTC GGTGCACATA TTCTATGTGG
-------------------------------------------------------------------------------
4801  TGCAAAGGCG GCACAACCCC AGTGCCACGT TGTGAGTTGG ATAGTTGTGG
      ACGTTTCCGC CGTGTTGGGG TCACGGTGCA ACACTCAACC TATCAACACC
-------------------------------------------------------------------------------
4851  AAAGAGTCAA ATGGCTCTCC TCAAGCGTAT TCAACAAGGG GCTGAAGGAT
      TTTCTCAGTT TACCGAGAGG AGTTCGCATA AGTTGTTCCC CGACTTCCTA
-------------------------------------------------------------------------------
4901  GCCCAGAAGG TACCCCATTG TATGGGATCT GATCTGGGGC CTCGGTGCAC
      CGGGTCTTCC ATGGGGTAAC ATACCCTAGA CTAGACCCCG GAGCCACGTG
-------------------------------------------------------------------------------
4951  ATGCTTTACA TGTGTTTAGT CGAGGTTAAA AAACGTCTAG GCCCCCCGAA
      TACGAAATGT ACACAAATCA GCTCCAATTT TTTGCAGATC CGGGGGGCTT
-------------------------------------------------------------------------------
5001  CCACGGGGAC GTGGTTTTCC TTTGAAAAAC ACGATGATAA TACCATGATT
      GGTGCCCCTG CACCAAAAGG AAACTTTTTG TGCTACTATT ATGGTACTAA
-------------------------------------------------------------------------------
5051  GAACAAGATG GATTGCACGC AGGTTCTCCG GCCGCTTGGG TGGAGAGGCT
      CTTGTTCTAC CTAACGTGCG TCCAAGAGGC CGGCGAACCC ACCTCTCCGA
-------------------------------------------------------------------------------
5101  ATTCGGCTAT GACTGGGCAC AACAGACAAT CGGCTGCTCT GATGCCGCCG
      TAAGCCGATA CTGACCCGTG TTGTCTGTTA GCCGACGAGA CTACGGCGGC
-------------------------------------------------------------------------------
5151  TGTTCCGGCT GTCAGCGCAG GGGCGCCCGG TTCTTTTTGT CAAGACCGAC
      ACAAGGCCGA CAGTCGCGTC CCCGCGGGCC AAGAAAAACA GTTCTGGCTG
-------------------------------------------------------------------------------
5201  CTGTCCGGTG CCCTGAATGA ACTGCAGGAC GAGGCAGCGC GGCTATCGTG
      GACAGGCCAC GGGACTTACT TGACGTCCTG CTCCGTCGCG CCGATAGCAC
-------------------------------------------------------------------------------
5251  GCTGGCCACG ACGGGCGTTC CTTGCGCAGC TGTGCTCGAC GTTGTCACTG
      CGACCGGTGC TGCCCGCAAG GAACGCGTCG ACACGAGCTG CAACAGTGAC
-------------------------------------------------------------------------------
5301  AAGCGGGAAG GGACTGGCTG CTATTGGGCG AAGTGCCGGG GCAGGATCTC
      TTCGCCCTTC CCTGACCGAC GATAACCCGC TTCACGGCCC CGTCCTAGAG
-------------------------------------------------------------------------------
5351  CTGTCATCTC ACCTTGCTCC TGCCGAGAAA GTATCCATCA TGGCTGATGC
      GACAGTAGAG TGGAACGAGG ACGGCTCTTT CATAGGTAGT ACCGACTACG
-------------------------------------------------------------------------------
5401  AATGCGGCGG CTGCATACGC TTGATCCGGC TACCTGCCCA TTCGACCACC
      TTACGCCGCC GACGTATGCG AACTAGGCCG ATGGACGGGT AAGCTGGTGG
-------------------------------------------------------------------------------
5451  AAGCGAAACA TCGCATCGAG CGAGCACGTA CTCGGATGGA AGCCGGTCTT
      TTCGCTTTGT AGCGTAGCTC GCTCGTGCAT GAGCCTACCT TCGGCCAGAA
-------------------------------------------------------------------------------
5501  GTCGATCAGG ATGATCTGGA CGAAGAGCAT CAGGGGCTCG CGCCAGCCGA
      CAGCTAGTCC TACTAGACCT GCTTCTCGTA GTCCCCGAGC GCGGTCGGCT
-------------------------------------------------------------------------------
5551  ACTGTTCGCC AGGCTCAAGG CGCGCATGCC CGACGGCGAG GATCTCGTCG
      TGACAAGCGG TCCGAGTTCC GCGCGTACGG GCTGCCGCTC CTAGAGCAGC
-------------------------------------------------------------------------------
5601  TGACCCATGG CGATGCCTGC TTGCCGAATA TCATGGTGGA AAATGGCCGC
      ACTGGGTACC GCTACGGACG AACGGCTTAT AGTACCACCT TTTACCGGCG
-------------------------------------------------------------------------------
5651  TTTTCTGGAT TCATCGACTG TGGCCGGCTG GGTGTGGCGG ACCGCTATCA
      AAAAGACCTA AGTAGCTGAC ACCGGCCGAC CCACACCGCC TGGCGATAGT
-------------------------------------------------------------------------------
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```
5701  GGACATAGCG TTGGCTACCC GTGATATTGC TGAAGAGCTT GGCGGCGAAT
      CCTGTATCGC AACCGATGGG CACTATAACG ACTTCTCGAA CCGCCGCTTA
-------------------------------------------------------------------------------
5751  GGGCTGACCG CTTCCTCGTG CTTTACGGTA TCGCCGCTCC CGATTCGCAG
      CCCGACTGGC GAAGGAGCAC GAAATGCCAT AGCGGCGAGG GCTAAGCGTC
-------------------------------------------------------------------------------
5801  CGCATCGCCT TCTATCGCCT TCTTGACGAG TTCTTCTGAG CGGGACTCTG
      GCGTAGCGGA AGATAGCGGA AGAACTGCTC AAGAAGACTC GCCCTGAGAC
-------------------------------------------------------------------------------
5851  GGGTTCGCAT CGATAAAATA AAAGATTTTA TTTAGTCTCC AGAAAAAGGG
      CCCAAGCGTA GCTATTTTAT TTTCTAAAAT AAATCAGAGG TCTTTTTCCC
-------------------------------------------------------------------------------
5901  GGGAATGAAA GACCCCACCT GTAGGTTTGG CAAGCTAGCT TAAGTAACGC
      CCCTTACTTT CTGGGGTGGA CATCCAAACC GTTCGATCGA ATTCATTGCG
-------------------------------------------------------------------------------
5951  CATTTTGCAA GGCATGGAAA AATACATAAC TGAGAATAGA GAAGTTCAGA
      GTAAAACGTT CCGTACCTTT TTATGTATTG ACTCTTATCT CTTCAAGTCT
-------------------------------------------------------------------------------
6001  TCAAGGTCAG GAACAGATGG AACAGCTGAA TATGGGCCAA ACAGGATATC
      AGTTCCAGTC CTTGTCTACC TTGTCGACTT ATACCCGGTT TGTCCTATAG
-------------------------------------------------------------------------------
6051  TGTGGTAAGC AGTTCCTGCC CCGGCTCAGG GCCAAGAACA GATGGAACAG
      ACACCATTCG TCAAGGACGG GGCCGAGTCC CGGTTCTTGT CTACCTTGTC
-------------------------------------------------------------------------------
6101  CTGAATATGG GCCAAACAGG ATATCTGTGG TAAGCAGTTC CTGCCCCGGC
      GACTTATACC CGGTTTGTCC TATAGACACC ATTCGTCAAG GACGGGGCCG
-------------------------------------------------------------------------------
6151  TCAGGGCCAA GAACAGATGG TCCCCAGATG CGGTCCAGCC CTCAGCAGTT
      AGTCCCGGTT CTTGTCTACC AGGGGTCTAC GCCAGGTCGG GAGTCGTCAA
-------------------------------------------------------------------------------
6201  TCTAGAGAAC CATCAGATGT TTCCAGGGTG CCCCAAGGAC CTGAAATGAC
      AGATCTCTTG GTAGTCTACA AAGGTCCCAC GGGGTTCCTG GACTTTACTG
-------------------------------------------------------------------------------
6251  CCTGTGCCTT ATTTGAACTA ACCAATCAGT TCGCTTCTCG CTTCTGTTCG
      GGACACGGAA TAAACTTGAT TGGTTAGTCA AGCGAAGAGC GAAGACAAGC
-------------------------------------------------------------------------------
6301  CGCGCTTCTG CTCCCCGAGC TCAATAAAAG AGCCCACAAC CCCTCACTCG
      GCGCGAAGAC GAGGGGCTCG AGTTATTTTC TCGGGTGTTG GGGAGTGAGC
-------------------------------------------------------------------------------
6351  GGGCGCCAGT CCTCCGATTG ACTGAGTCGC CCGGGTACCC GTGTATCCAA
      CCCGCGGTCA GGAGGCTAAC TGACTCAGCG GGCCCATGGG CACATAGGTT
-------------------------------------------------------------------------------
6401  TAAACCCTCT TGCAGTTGCA TCCGACTTGT GGTCTCGCTG TTCCTTGGGA
      ATTTGGGAGA ACGTCAACGT AGGCTGAACA CCAGAGCGAC AAGGAACCCT
-------------------------------------------------------------------------------
6451  GGGTCTCCTC TGAGTGATTG ACTACCCGTC AGCGGGGGTC TTTCATTCAT
      CCCAGAGGAG ACTCACTAAC TGATGGGCAG TCGCCCCCAG AAAGTAAGTA
-------------------------------------------------------------------------------
6501  GCAGCATGTA TCAAAATTAA TTTGGTTTTT TTTCTTAAGT ATTTACATTA
      CGTCGTACAT AGTTTTAATT AAACCAAAAA AAAGAATTCA TAAATGTAAT
-------------------------------------------------------------------------------
6551  AATGGCCATA GTTGCATTAA TGAATCGGCC AACGCGCGGG GAGAGGCGGT
      TTACCGGTAT CAACGTAATT ACTTAGCCGG TTGCGCGCCC CTCTCCGCCA
-------------------------------------------------------------------------------
6601  TTGCGTATTG GCGCTCTTCC GCTTCCTCGC TCACTGACTC GCTGCGCTCG
      AACGCATAAC CGCGAGAAGG CGAAGGAGCG AGTGACTGAG CGACGCGAGC
-------------------------------------------------------------------------------
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```
6651  GTCGTTCGGC TGCGGCGAGC GGTATCAGCT CACTCAAAGG CGGTAATACG
      CAGCAAGCCG ACGCCGCTCG CCATAGTCGA GTGAGTTTCC GCCATTATGC
-------------------------------------------------------------------------------
6701  GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAG
      CAATAGGTGT CTTAGTCCCC TATTGCGTCC TTTCTTGTAC ACTCGTTTTC
-------------------------------------------------------------------------------
6751  GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC
      CGGTCGTTTT CCGGTCCTTG GCATTTTTCC GGCGCAACGA CCGCAAAAAG
-------------------------------------------------------------------------------
6801  CATAGGCTCC GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA
      GTATCCGAGG CGGGGGGACT GCTCGTAGTG TTTTTAGCTG CGAGTTCAGT
-------------------------------------------------------------------------------
6851  GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG
      CTCCACCGCT TTGGGCTGTC CTGATATTTC TATGGTCCGC AAAGGGGGAC
-------------------------------------------------------------------------------
6901  GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC
      CTTCGAGGGA GCACGCGAGA GGACAAGGCT GGGACGGCGA ATGGCCTATG
-------------------------------------------------------------------------------
6951  CTGTCCGCCT TTCTCCCTTC GGGAAGCGTG GCGCTTTCTC ATAGCTCACG
      GACAGGCGGA AAGAGGGAAG CCCTTCGCAC CGCGAAAGAG TATCGAGTGC
-------------------------------------------------------------------------------
7001  CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG
      GACATCCATA GAGTCAAGCC ACATCCAGCA AGCGAGGTTC GACCCGACAC
-------------------------------------------------------------------------------
7051  TGCACGAACC CCCCGTTCAG CCCGACCGCT GCGCCTTATC CGGTAACTAT
      ACGTGCTTGG GGGGCAAGTC GGGCTGGCGA CGCGGAATAG GCCATTGATA
-------------------------------------------------------------------------------
7101  CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC
      GCAGAACTCA GGTTGGGCCA TTCTGTGCTG AATAGCGGTG ACCGTCGTCG
-------------------------------------------------------------------------------
7151  CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT
      GTGACCATTG TCCTAATCGT CTCGCTCCAT ACATCCGCCA CGATGTCTCA
-------------------------------------------------------------------------------
7201  TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGAAC AGTATTTGGT
      AGAACTTCAC CACCGGATTG ATGCCGATGT GATCTTCTTG TCATAAACCA
-------------------------------------------------------------------------------
7251  ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC
      TAGACGCGAG ACGACTTCGG TCAATGGAAG CCTTTTTCTC AACCATCGAG
-------------------------------------------------------------------------------
7301  TTGATCCGGC AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA
      AACTAGGCCG TTTGTTTGGT GGCGACCATC GCCACCAAAA AAACAAACGT
-------------------------------------------------------------------------------
7351  AGCAGCAGAT TACGCGCAGA AAAAAAGGAT CTCAAGAAGA TCCTTTGATC
      TCGTCGTCTA ATGCGCGTCT TTTTTTCCTA GAGTTCTTCT AGGAAACTAG
-------------------------------------------------------------------------------
7401  TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT
      AAAAGATGCC CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA
-------------------------------------------------------------------------------
7451  TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTGCGGC
      AAACCAGTAC TCTAATAGTT TTTCCTAGAA GTGGATCTAG GAAAACGCCG
-------------------------------------------------------------------------------
7501  CGCAAATCAA TCTAAAGTAT ATATGAGTAA ACTTGGTCTG ACAGTTACCA
      GCGTTTAGTT AGATTTCATA TATACTCATT TGAACCAGAC TGTCAATGGT
-------------------------------------------------------------------------------
7551  ATGCTTAATC AGTGAGGCAC CTATCTCAGC GATCTGTCTA TTTCGTTCAT
      TACGAATTAG TCACTCCGTG GATAGAGTCG CTAGACAGAT AAAGCAAGTA
-------------------------------------------------------------------------------
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```
7601  CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC
      GGTATCAACG GACTGAGGGG CAGCACATCT ATTGATGCTA TGCCCTCCCG
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7651  TTACCATCTG GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGCTCACC
      AATGGTAGAC CGGGGTCACG ACGTTACTAT GGCGCTCTGG GTGCGAGTGG
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7701  GGCTCCAGAT TTATCAGCAA TAAACCAGCC AGCCGGAAGG GCCGAGCGCA
      CCGAGGTCTA AATAGTCGTT ATTTGGTCGG TCGGCCTTCC CGGCTCGCGT
-------------------------------------------------------------------------------
7751  GAAGTGGTCC TGCAACTTTA TCCGCCTCCA TCCAGTCTAT TAATTGTTGC
      CTTCACCAGG ACGTTGAAAT AGGCGGAGGT AGGTCAGATA ATTAACAACG
-------------------------------------------------------------------------------
7801  CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC GCAACGTTGT
      GCCCTTCGAT CTCATTCATC AAGCGGTCAA TTATCAAACG CGTTGCAACA
-------------------------------------------------------------------------------
7851  TGCCATTGCT ACAGGCATCG TGGTGTCACG CTCGTCGTTT GGTATGGCTT
      ACGGTAACGA TGTCCGTAGC ACCACAGTGC GAGCAGCAAA CCATACCGAA
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7901  CATTCAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG
      GTAAGTCGAG GCCAAGGGTT GCTAGTTCCG CTCAATGTAC TAGGGGGTAC
-------------------------------------------------------------------------------
7951  TTGTGCAAAA AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG
      AACACGTTTT TTCGCCAATC GAGGAAGCCA GGAGGCTAGC AACAGTCTTC
-------------------------------------------------------------------------------
8001  TAAGTTGGCC GCAGTGTTAT CACTCATGGT TATGGCAGCA CTGCATAATT
      ATTCAACCGG CGTCACAATA GTGAGTACCA ATACCGTCGT GACGTATTAA
-------------------------------------------------------------------------------
8051  CTCTTACTGT CATGCCATCC GTAAGATGCT TTTCTGTGAC TGGTGAGTAC
      GAGAATGACA GTACGGTAGG CATTCTACGA AAAGACACTG ACCACTCATG
-------------------------------------------------------------------------------
8101  TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA GTTGCTCTTG
      AGTTGGTTCA GTAAGACTCT TATCACATAC GCCGCTGGCT CAACGAGAAC
-------------------------------------------------------------------------------
8151  CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAAG
      GGGCCGCAGT TATGCCCTAT TATGGCGCGG TGTATCGTCT TGAAATTTTC
-------------------------------------------------------------------------------
8201  TGCTCATCAT TGGAAAACGT TCTTCGGGGC GAAAACTCTC AAGGATCTTA
      ACGAGTAGTA ACCTTTTGCA AGAAGCCCCG CTTTTGAGAG TTCCTAGAAT
-------------------------------------------------------------------------------
8251  CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC
      GGCGACAACT CTAGGTCAAG CTACATTGGG TGAGCACGTG GGTTGACTAG
-------------------------------------------------------------------------------
8301  TTCAGCATCT TTTACTTTCA CCAGCGTTTC TGGGTGAGCA AAAACAGGAA
      AAGTCGTAGA AAATGAAAGT GGTCGCAAAG ACCCACTCGT TTTTGTCCTT
-------------------------------------------------------------------------------
8351  GGCAAAATGC CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA
      CCGTTTTACG GCGTTTTTTC CCTTATTCCC GCTGTGCCTT TACAACTTAT
-------------------------------------------------------------------------------
8401  CTCATACTCT TCCTTTTTCA ATATTATTGA AGCATTTATC AGGGTTATTG
      GAGTATGAGA AGGAAAAAGT TATAATAACT TCGTAAATAG TCCCAATAAC
-------------------------------------------------------------------------------
8451  TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG
      AGAGTACTCG CCTATGTATA AACTTACATA AATCTTTTTA TTTGTTTATC
-------------------------------------------------------------------------------
8501  GGGTTCCGCG CACATTTC
      CCCAAGGCGC GTGTAAAG
-------------------------------------------------------------------------------
```

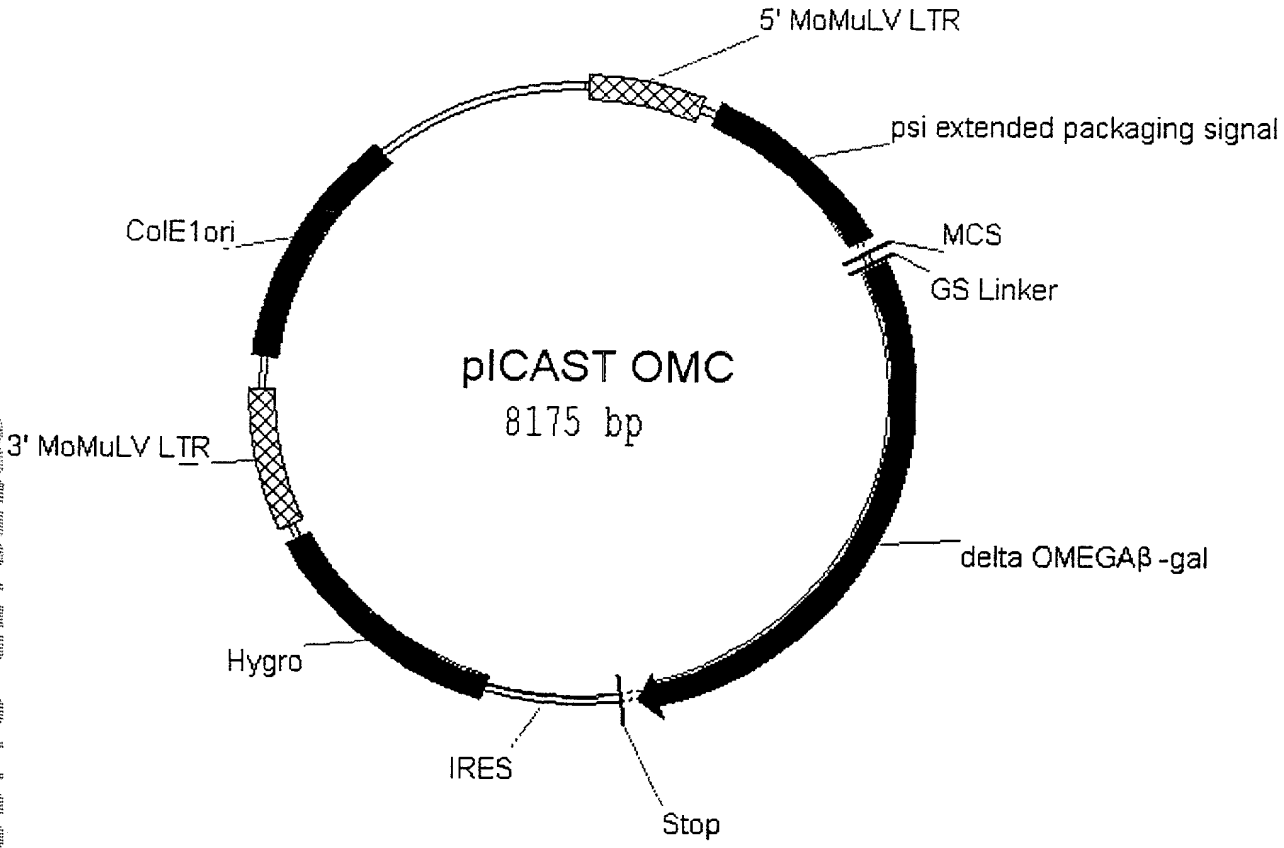
5' MoMuLV LTR
psi extended packaging signal
MCS
GS Linker
delta OMEGAβ -gal
Stop
IRES
Hygro
3' MoMuLV LTR
ColE1ori
pICAST OMC
8175 bp

Figure 12A

```
   1  CTGCAGCCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG
      GACGTCGGAC TTATACCCGG TTTGTCCTAT AGACACCATT CGTCAAGGAC
--------------------------------------------------------------------------------
  51  CCCCGGCTCA GGGCCAAGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA
      GGGGCCGAGT CCCGGTTCTT GTCTACCTTG TCGACTTATA CCCGGTTTGT
--------------------------------------------------------------------------------
 101  GGATATCTGT GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT
      CCTATAGACA CCATTCGTCA AGGACGGGGC CGAGTCCCGG TTCTTGTCTA
--------------------------------------------------------------------------------
 151  GGTCCCCAGA TGCGGTCCAG CCCTCAGCAG TTTCTAGAGA ACCATCAGAT
      CCAGGGGTCT ACGCCAGGTC GGGAGTCGTC AAAGATCTCT TGGTAGTCTA
--------------------------------------------------------------------------------
 201  GTTTCCAGGG TGCCCCAAGG ACCTGAAATG ACCCTGTGCC TTATTTGAAC
      CAAAGGTCCC ACGGGGTTCC TGGACTTTAC TGGGACACGG AATAAACTTG
--------------------------------------------------------------------------------
 251  TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC TGCTCCCCGA
      ATTGGTTAGT CAAGCGAAGA GCGAAGACAA GCGCGCGAAG ACGAGGGGCT
--------------------------------------------------------------------------------
 301  GCTCAATAAA AGAGCCCACA ACCCCTCACT CGGGGCGCCA GTCCTCCGAT
      CGAGTTATTT TCTCGGGTGT TGGGGAGTGA GCCCCGCGGT CAGGAGGCTA
--------------------------------------------------------------------------------
 351  TGACTGAGTC GCCCGGGTAC CCGTGTATCC AATAAACCCT CTTGCAGTTG
      ACTGACTCAG CGGGCCCATG GGCACATAGG TTATTTGGGA GAACGTCAAC
--------------------------------------------------------------------------------
 401  CATCCGACTT GTGGTCTCGC TGTTCCTTGG GAGGGTCTCC TCTGAGTGAT
      GTAGGCTGAA CACCAGAGCG ACAAGGAACC CTCCCAGAGG AGACTCACTA
--------------------------------------------------------------------------------
 451  TGACTACCCG TCAGCGGGGG TCTTTCATTT GGGGGCTCGT CCGGGATCGG
      ACTGATGGGC AGTCGCCCCC AGAAAGTAAA CCCCCGAGCA GGCCCTAGCC
--------------------------------------------------------------------------------
 501  GAGACCCCTG CCCAGGGACC ACCGACCCAC CACCGGGAGG CAAGCTGGCC
      CTCTGGGGAC GGGTCCCTGG TGGCTGGGTG GTGGCCCTCC GTTCGACCGG
--------------------------------------------------------------------------------
 551  AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG ACTGATTTTA
      TCGTTGAATA GACACAGACA GGCTAACAGA TCACAGATAC TGACTAAAAT
--------------------------------------------------------------------------------
 601  TGCGCCTGCG TCGGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC
      ACGCGGACGC AGCCATGATC AATCGATTGA TCGAGACATA GACCGCCTGG
--------------------------------------------------------------------------------
 651  CGTGGTGGAA CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG
      GCACCACCTT GACTGCTCAA GACTTGTGGG CCGGCGTTGG GACCCTCTGC
--------------------------------------------------------------------------------
 701  TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG CCCGACCTGA GGAAGGGAGT
      AGGGTCCCTG AAACCCCCGG CAAAAACACC GGGCTGGACT CCTTCCCTCA
--------------------------------------------------------------------------------
 751  CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT AGGAGACGAG
      GCTACACCTT AGGCTGGGGC AGTCCTATAC ACCAAGACCA TCCTCTGCTC
--------------------------------------------------------------------------------
 801  AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA
      TTGGATTTTG TCAAGGGCGG AGGCAGACTT AAAAACGAAA GCCAAACCTT
--------------------------------------------------------------------------------
 851  CCGAAGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT
      GGCTTCGGCG CGCAGAACAG ACGACGTCGT AGCAAGACAC AACAGAGACA
--------------------------------------------------------------------------------
 901  CTGACTGTGT TTCTGTATTT GTCTGAAAAT TAGGGCCAGA CTGTTACCAC
      GACTGACACA AAGACATAAA CAGACTTTTA ATCCCGGTCT GACAATGGTG
--------------------------------------------------------------------------------
```

FIGURE 12B

```
 951  TCCCTTAAGT TTGACCTTAG GTAACTGGAA AGATGTCGAG CGGCTCGCTC
      AGGGAATTCA AACTGGAATC CATTGACCTT TCTACAGCTC GCCGAGCGAG
-------------------------------------------------------------------------------
1001  ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
      TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
-------------------------------------------------------------------------------
1051  GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
      CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
-------------------------------------------------------------------------------
1101  CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
      GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
-------------------------------------------------------------------------------
1151  ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
      TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
-------------------------------------------------------------------------------
1201  TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
      AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
-------------------------------------------------------------------------------
1251  TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
      AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
-------------------------------------------------------------------------------
1301  CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
      GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
-------------------------------------------------------------------------------
1351  GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAATCAGG
      CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTAGTCC
-------------------------------------------------------------------------------
1401  CCTTGGCGCG CCGGATCCTT AATTAAGCGC AATTGGGAGG TGGCGGTAGC
      GGAACCGCGC GGCCTAGGAA TTAATTCGCG TTAACCCTCC ACCGCCATCG
-------------------------------------------------------------------------------
1451  CTCGAGATGG GCGTGATTAC GGATTCACTG GCCGTCGTTT TACAACGTCG
      GAGCTCTACC CGCACTAATG CCTAAGTGAC CGGCAGCAAA ATGTTGCAGC
-------------------------------------------------------------------------------
1501  TGACTGGGAA AACCCTGGCG TTACCCAACT TAATCGCCTT GCAGCACATC
      ACTGACCCTT TTGGGACCGC AATGGGTTGA ATTAGCGGAA CGTCGTGTAG
-------------------------------------------------------------------------------
1551  CCCCTTTCGC CAGCTGGCGT AATAGCGAAG AGGCCCGCAC CGATCGCCCT
      GGGGAAAGCG GTCGACCGCA TTATCGCTTC TCCGGGCGTG GCTAGCGGGA
-------------------------------------------------------------------------------
1601  TCCCAACAGT TACGCAGCCT GAATGGCGAA TGGCGCTTTG CCTGGTTTCC
      AGGGTTGTCA ATGCGTCGGA CTTACCGCTT ACCGCGAAAC GGACCAAAGG
-------------------------------------------------------------------------------
1651  GGCACCAGAA GCGGTGCCGG AAAGCTGGCT GGAGTGCGAT CTTCCTGAGG
      CCGTGGTCTT CGCCACGGCC TTTCGACCGA CCTCACGCTA GAAGGACTCC
-------------------------------------------------------------------------------
1701  CCGATACTGT CGTCGTCCCC TCAAACTGGC AGATGCACGG TTACGATGCG
      GGCTATGACA GCAGCAGGGG AGTTTGACCG TCTACGTGCC AATGCTACGC
-------------------------------------------------------------------------------
1751  CCCATCTACA CCAACGTGAC CTATCCCATT ACGGTCAATC CGCCGTTTGT
      GGGTAGATGT GGTTGCACTG GATAGGGTAA TGCCAGTTAG GCGGCAAACA
-------------------------------------------------------------------------------
1801  TCCCACGGAG AATCCGACGG GTTGTTACTC GCTCACATTT AATGTTGATG
      AGGGTGCCTC TTAGGCTGCC CAACAATGAG CGAGTGTAAA TTACAACTAC
-------------------------------------------------------------------------------
1851  AAAGCTGGCT ACAGGAAGGC CAGACGCGAA TTATTTTTGA TGGCGTTAAC
      TTTCGACCGA TGTCCTTCCG GTCTGCGCTT AATAAAAACT ACCGCAATTG
-------------------------------------------------------------------------------
```

```
1901  TCGGCGTTTC ATCTGTGGTG CAACGGGCGC TGGGTCGGTT ACGGCCAGGA
      AGCCGCAAAG TAGACACCAC GTTGCCCGCG ACCCAGCCAA TGCCGGTCCT
-------------------------------------------------------------------------------
1951  CAGTCGTTTG CCGTCTGAAT TTGACCTGAG CGCATTTTTA CGCGCCGGAG
      GTCAGCAAAC GGCAGACTTA AACTGGACTC GCGTAAAAAT GCGCGGCCTC
-------------------------------------------------------------------------------
2001  AAAACCGCCT CGCGGTGATG GTGCTGCGCT GGAGTGACGG CAGTTATCTG
      TTTTGGCGGA GCGCCACTAC CACGACGCGA CCTCACTGCC GTCAATAGAC
-------------------------------------------------------------------------------
2051  GAAGATCAGG ATATGTGGCG GATGAGCGGC ATTTTCCGTG ACGTCTCGTT
      CTTCTAGTCC TATACACCGC CTACTCGCCG TAAAAGGCAC TGCAGAGCAA
-------------------------------------------------------------------------------
2101  GCTGCATAAA CCGACTACAC AAATCAGCGA TTTCCATGTT GCCACTCGCT
      CGACGTATTT GGCTGATGTG TTTAGTCGCT AAAGGTACAA CGGTGAGCGA
-------------------------------------------------------------------------------
2151  TTAATGATGA TTTCAGCCGC GCTGTACTGG AGGCTGAAGT TCAGATGTGC
      AATTACTACT AAAGTCGGCG CGACATGACC TCCGACTTCA AGTCTACACG
-------------------------------------------------------------------------------
2201  GGCGAGTTGC GTGACTACCT ACGGGTAACA GTTTCTTTAT GGCAGGGTGA
      CCGCTCAACG CACTGATGGA TGCCCATTGT CAAAGAAATA CCGTCCCACT
-------------------------------------------------------------------------------
2251  AACGCAGGTC GCCAGCGGCA CCGCGCCTTT CGGCGGTGAA ATTATCGATG
      TTGCGTCCAG CGGTCGCCGT GGCGCGGAAA GCCGCCACTT TAATAGCTAC
-------------------------------------------------------------------------------
2301  AGCGTGGTGG TTATGCCGAT CGCGTCACAC TACGTCTGAA CGTCGAAAAC
      TCGCACCACC AATACGGCTA GCGCAGTGTG ATGCAGACTT GCAGCTTTTG
-------------------------------------------------------------------------------
2351  CCGAAACTGT GGAGCGCCGA AATCCCGAAT CTCTATCGTG CGGTGGTTGA
      GGCTTTGACA CCTCGCGGCT TTAGGGCTTA GAGATAGCAC GCCACCAACT
-------------------------------------------------------------------------------
2401  ACTGCACACC GCCGACGGCA CGCTGATTGA AGCAGAAGCC TGCGATGTCG
      TGACGTGTGG CGGCTGCCGT GCGACTAACT TCGTCTTCGG ACGCTACAGC
-------------------------------------------------------------------------------
2451  GTTTCCGCGA GGTGCGGATT GAAAATGGTC TGCTGCTGCT GAACGGCAAG
      CAAAGGCGCT CCACGCCTAA CTTTTACCAG ACGACGACGA CTTGCCGTTC
-------------------------------------------------------------------------------
2501  CCGTTGCTGA TTCGAGGCGT TAACCGTCAC GAGCATCATC CTCTGCATGG
      GGCAACGACT AAGCTCCGCA ATTGGCAGTG CTCGTAGTAG GAGACGTACC
-------------------------------------------------------------------------------
2551  TCAGGTCATG GATGAGCAGA CGATGGTGCA GGATATCCTG CTGATGAAGC
      AGTCCAGTAC CTACTCGTCT GCTACCACGT CCTATAGGAC GACTACTTCG
-------------------------------------------------------------------------------
2601  AGAACAACTT TAACGCCGTG CGCTGTTCGC ATTATCCGAA CCATCCGCTG
      TCTTGTTGAA ATTGCGGCAC GCGACAAGCG TAATAGGCTT GGTAGGCGAC
-------------------------------------------------------------------------------
2651  TGGTACACGC TGTGCGACCG CTACGGCCTG TATGTGGTGG ATGAAGCCAA
      ACCATGTGCG ACACGCTGGC GATGCCGGAC ATACACCACC TACTTCGGTT
-------------------------------------------------------------------------------
2701  TATTGAAACC CACGGCATGG TGCCAATGAA TCGTCTGACC GATGATCCGC
      ATAACTTTGG GTGCCGTACC ACGGTTACTT AGCAGACTGG CTACTAGGCG
-------------------------------------------------------------------------------
2751  GCTGGCTACC GGCGATGAGC GAACGCGTAA CGCGAATGGT GCAGCGCGAT
      CGACCGATGG CCGCTACTCG CTTGCGCATT GCGCTTACCA CGTCGCGCTA
-------------------------------------------------------------------------------
2801  CGTAATCACC CGAGTGTGAT CATCTGGTCG CTGGGGAATG AATCAGGCCA
      GCATTAGTGG GCTCACACTA GTAGACCAGC GACCCCTTAC TTAGTCCGGT
-------------------------------------------------------------------------------
```

```
2851  CGGCGCTAAT CACGACGCGC TGTATCGCTG GATCAAATCT GTCGATCCTT
      GCCGCGATTA GTGCTGCGCG ACATAGCGAC CTAGTTTAGA CAGCTAGGAA
-------------------------------------------------------------------------------
2901  CCCGCCCGGT GCAGTATGAA GGCGGCGGAG CCGACACCAC GGCCACCGAT
      GGGCGGGCCA CGTCATACTT CCGCCGCCTC GGCTGTGGTG CCGGTGGCTA
-------------------------------------------------------------------------------
2951  ATTATTTGCC CGATGTACGC GCGCGTGGAT GAAGACCAGC CCTTCCCGGC
      TAATAAACGG GCTACATGCG CGCGCACCTA CTTCTGGTCG GGAAGGGCCG
-------------------------------------------------------------------------------
3001  TGTGCCGAAA TGGTCCATCA AAAAATGGCT TTCGCTACCT GGAGAGACGC
      ACACGGCTTT ACCAGGTAGT TTTTTACCGA AAGCGATGGA CCTCTCTGCG
-------------------------------------------------------------------------------
3051  GCCCGCTGAT CCTTTGCGAA TACGCCCACG CGATGGGTAA CAGTCTTGGC
      CGGGCGACTA GGAAACGCTT ATGCGGGTGC GCTACCCATT GTCAGAACCG
-------------------------------------------------------------------------------
3101  GGTTTCGCTA AATACTGGCA GGCGTTTCGT CAGTATCCCC GTTTACAGGG
      CCAAAGCGAT TTATGACCGT CCGCAAAGCA GTCATAGGGG CAAATGTCCC
-------------------------------------------------------------------------------
3151  CGGCTTCGTC TGGGACTGGG TGGATCAGTC GCTGATTAAA TATGATGAAA
      GCCGAAGCAG ACCCTGACCC ACCTAGTCAG CGACTAATTT ATACTACTTT
-------------------------------------------------------------------------------
3201  ACGGCAACCC GTGGTCGGCT TACGGCGGTG ATTTTGGCGA TACGCCGAAC
      TGCCGTTGGG CACCAGCCGA ATGCCGCCAC TAAAACCGCT ATGCGGCTTG
-------------------------------------------------------------------------------
3251  GATCGCCAGT TCTGTATGAA CGGTCTGGTC TTTGCCGACC GCACGCCGCA
      CTAGCGGTCA AGACATACTT GCCAGACCAG AAACGGCTGG CGTGCGGCGT
-------------------------------------------------------------------------------
3301  TCCAGCGCTG ACGGAAGCAA AACACCAGCA GCAGTTTTTC CAGTTCCGTT
      AGGTCGCGAC TGCCTTCGTT TTGTGGTCGT CGTCAAAAAG GTCAAGGCAA
-------------------------------------------------------------------------------
3351  TATCCGGGCA AACCATCGAA GTGACCAGCG AATACCTGTT CCGTCATAGC
      ATAGGCCCGT TTGGTAGCTT CACTGGTCGC TTATGGACAA GGCAGTATCG
-------------------------------------------------------------------------------
3401  GATAACGAGC TCCTGCACTG GATGGTGGCG CTGGATGGTA AGCCGCTGGC
      CTATTGCTCG AGGACGTGAC CTACCACCGC GACCTACCAT TCGGCGACCG
-------------------------------------------------------------------------------
3451  AAGCGGTGAA GTGCCTCTGG ATGTCGCTCC ACAAGGTAAA CAGTTGATTG
      TTCGCCACTT CACGGAGACC TACAGCGAGG TGTTCCATTT GTCAACTAAC
-------------------------------------------------------------------------------
3501  AACTGCCTGA ACTACCGCAG CCGGAGAGCG CCGGGCAACT CTGGCTCACA
      TTGACGGACT TGATGGCGTC GGCCTCTCGC GGCCCGTTGA GACCGAGTGT
-------------------------------------------------------------------------------
3551  GTACGCGTAG TGCAACCGAA CGCGACCGCA TGGTCAGAAG CCGGGCACAT
      CATGCGCATC ACGTTGGCTT GCGCTGGCGT ACCAGTCTTC GGCCCGTGTA
-------------------------------------------------------------------------------
3601  CAGCGCCTGG CAGCAGTGGC GTCTGGCGGA AAACCTCAGT GTGACGCTCC
      GTCGCGGACC GTCGTCACCG CAGACCGCCT TTTGGAGTCA CACTGCGAGG
-------------------------------------------------------------------------------
3651  CCGCCGCGTC CCACGCCATC CCGCATCTGA CCACCAGCGA AATGGATTTT
      GGCGGCGCAG GGTGCGGTAG GGCGTAGACT GGTGGTCGCT TTACCTAAAA
-------------------------------------------------------------------------------
3701  TGCATCGAGC TGGGTAATAA GCGTTGGCAA TTTAACCGCC AGTCAGGCTT
      ACGTAGCTCG ACCCATTATT CGCAACCGTT AAATTGGCGG TCAGTCCGAA
-------------------------------------------------------------------------------
3751  TCTTTCACAG ATGTGGATTG GCGATAAAAA ACAACTGCTG ACGCCGCTGC
      AGAAAGTGTC TACACCTAAC CGCTATTTTT TGTTGACGAC TGCGGCGACG
-------------------------------------------------------------------------------
```

```
3801  GCGATCAGTT CACCCGTGTC GATAGATCTG AACAGAAACT CATTTCCGAA
      CGCTAGTCAA GTGGGCACAG CTATCTAGAC TTGTCTTTGA GTAAAGGCTT
-------------------------------------------------------------------------------
3851  GAAGACCTAG TCGACCATCA TCATCATCAT CACCGGTAAT AATAGGTAGA
      CTTCTGGATC AGCTGGTAGT AGTAGTAGTA GTGGCCATTA TTATCCATCT
-------------------------------------------------------------------------------
3901  TAAGTGACTG ATTAGATGCA TTTCGACTAG ATCCCTCGAC CAATTCCGGT
      ATTCACTGAC TAATCTACGT AAAGCTGATC TAGGGAGCTG GTTAAGGCCA
-------------------------------------------------------------------------------
3951  TATTTTCCAC CATATTGCCG TCTTTTGGCA ATGTGAGGGC CCGGAAACCT
      ATAAAAGGTG GTATAACGGC AGAAAACCGT TACACTCCCG GGCCTTTGGA
-------------------------------------------------------------------------------
4001  GGCCCTGTCT TCTTGACGAG CATTCCTAGG GGTCTTTCCC CTCTCGCCAA
      CCGGGACAGA AGAACTGCTC GTAAGGATCC CCAGAAAGGG GAGAGCGGTT
-------------------------------------------------------------------------------
4051  AGGAATGCAA GGTCTGTTGA ATGTCGTGAA GGAAGCAGTT CCTCTGGAAG
      TCCTTACGTT CCAGACAACT TACAGCACTT CCTTCGTCAA GGAGACCTTC
-------------------------------------------------------------------------------
4101  CTTCTTGAAG ACAAACAACG TCTGTAGCGA CCCTTTGCAG GCAGCGGAAC
      GAAGAACTTC TGTTTGTTGC AGACATCGCT GGGAAACGTC CGTCGCCTTG
-------------------------------------------------------------------------------
4151  CCCCCACCTG GCGACAGGTG CCTCTGCGGC CAAAAGCCAC GTGTATAAGA
      GGGGGTGGAC CGCTGTCCAC GGAGACGCCG GTTTTCGGTG CACATATTCT
-------------------------------------------------------------------------------
4201  TACACCTGCA AAGGCGGCAC AACCCCAGTG CCACGTTGTG AGTTGGATAG
      ATGTGGACGT TTCCGCCGTG TTGGGGTCAC GGTGCAACAC TCAACCTATC
-------------------------------------------------------------------------------
4251  TTGTGGAAAG AGTCAAATGG CTCTCCTCAA GCGTATTCAA CAAGGGGCTG
      AACACCTTTC TCAGTTTACC GAGAGGAGTT CGCATAAGTT GTTCCCCGAC
-------------------------------------------------------------------------------
4301  AAGGATGCCC AGAAGGTACC CCATTGTATG GGATCTGATC TGGGGCCTCG
      TTCCTACGGG TCTTCCATGG GGTAACATAC CCTAGACTAG ACCCCGGAGC
-------------------------------------------------------------------------------
4351  GTGCACATGC TTTACATGTG TTTAGTCGAG GTTAAAAAAC GTCTAGGCCC
      CACGTGTACG AAATGTACAC AAATCAGCTC CAATTTTTTG CAGATCCGGG
-------------------------------------------------------------------------------
4401  CCCGAACCAC GGGGACGTGG TTTTCCTTTG AAAAACACGA TGATAATACC
      GGGCTTGGTG CCCCTGCACC AAAAGGAAAC TTTTTGTGCT ACTATTATGG
-------------------------------------------------------------------------------
4451  ATGAAAAAGC CTGAACTCAC CGCGACGTCT GTCGAGAAGT TTCTGATCGA
      TACTTTTTCG GACTTGAGTG GCGCTGCAGA CAGCTCTTCA AAGACTAGCT
-------------------------------------------------------------------------------
4501  AAAGTTCGAC AGCGTCTCCG ACCTGATGCA GCTCTCGGAG GGCGAAGAAT
      TTTCAAGCTG TCGCAGAGGC TGGACTACGT CGAGAGCCTC CCGCTTCTTA
-------------------------------------------------------------------------------
4551  CTCGTGCTTT CAGCTTCGAT GTAGGAGGGC GTGGATATGT CCTGCGGGTA
      GAGCACGAAA GTCGAAGCTA CATCCTCCCG CACCTATACA GGACGCCCAT
-------------------------------------------------------------------------------
4601  AATAGCTGCG CCGATGGTTT CTACAAAGAT CGTTATGTTT ATCGGCACTT
      TTATCGACGC GGCTACCAAA GATGTTTCTA GCAATACAAA TAGCCGTGAA
-------------------------------------------------------------------------------
4651  TGCATCGGCC GCGCTCCCGA TTCCGGAAGT GCTTGACATT GGGGAATTTA
      ACGTAGCCGG CGCGAGGGCT AAGGCCTTCA CGAACTGTAA CCCCTTAAAT
-------------------------------------------------------------------------------
4701  GCGAGAGCCT GACCTATTGC ATCTCCCGCC GTGCACAGGG TGTCACGTTG
      CGCTCTCGGA CTGGATAACG TAGAGGGCGG CACGTGTCCC ACAGTGCAAC
-------------------------------------------------------------------------------
```

```
4751  CAAGACCTGC CTGAAACCGA ACTGCCCGCT GTTCTGCAGC CGGTCGCGGA
      GTTCTGGACG GACTTTGGCT TGACGGGCGA CAAGACGTCG GCCAGCGCCT
-------------------------------------------------------------------------------
4801  GGCCATGGAT GCGATCGCTG CGGCCGATCT TAGCCAGACG AGCGGGTTCG
      CCGGTACCTA CGCTAGCGAC GCCGGCTAGA ATCGGTCTGC TCGCCCAAGC
-------------------------------------------------------------------------------
4851  GCCCATTCGG ACCGCAAGGA ATCGGTCAAT ACACTACATG GCGTGATTTC
      CGGGTAAGCC TGGCGTTCCT TAGCCAGTTA TGTGATGTAC CGCACTAAAG
-------------------------------------------------------------------------------
4901  ATATGCGCGA TTGCTGATCC CCATGTGTAT CACTGGCAAA CTGTGATGGA
      TATACGCGCT AACGACTAGG GGTACACATA GTGACCGTTT GACACTACCT
-------------------------------------------------------------------------------
4951  CGACACCGTC AGTGCGTCCG TCGCGCAGGC TCTCGATGAG CTGATGCTTT
      GCTGTGGCAG TCACGCAGGC AGCGCGTCCG AGAGCTACTC GACTACGAAA
-------------------------------------------------------------------------------
5001  GGGCCGAGGA CTGCCCCGAA GTCCGGCACC TCGTGCACGC GGATTTCGGC
      CCCGGCTCCT GACGGGGCTT CAGGCCGTGG AGCACGTGCG CCTAAAGCCG
-------------------------------------------------------------------------------
5051  TCCAACAATG TCCTGACGGA CAATGGCCGC ATAACAGCGG TCATTGACTG
      AGGTTGTTAC AGGACTGCCT GTTACCGGCG TATTGTCGCC AGTAACTGAC
-------------------------------------------------------------------------------
5101  GAGCGAGGCG ATGTTCGGGG ATTCCCAATA CGAGGTCGCC AACATCTTCT
      CTCGCTCCGC TACAAGCCCC TAAGGGTTAT GCTCCAGCGG TTGTAGAAGA
-------------------------------------------------------------------------------
5151  TCTGGAGGCC GTGGTTGGCT TGTATGGAGC AGCAGACGCG CTACTTCGAG
      AGACCTCCGG CACCAACCGA ACATACCTCG TCGTCTGCGC GATGAAGCTC
-------------------------------------------------------------------------------
5201  CGGAGGCATC CGGAGCTTGC AGGATCGCCG CGGCTCCGGG CGTATATGCT
      GCCTCCGTAG GCCTCGAACG TCCTAGCGGC GCCGAGGCCC GCATATACGA
-------------------------------------------------------------------------------
5251  CCGCATTGGT CTTGACCAAC TCTATCAGAG CTTGGTTGAC GGCAATTTCG
      GGCGTAACCA GAACTGGTTG AGATAGTCTC GAACCAACTG CCGTTAAAGC
-------------------------------------------------------------------------------
5301  ATGATGCAGC TTGGGCGCAG GGTCGATGCG ACGCAATCGT CCGATCCGGA
      TACTACGTCG AACCCGCGTC CCAGCTACGC TGCGTTAGCA GGCTAGGCCT
-------------------------------------------------------------------------------
5351  GCCGGGACTG TCGGGCGTAC ACAAATCGCC CGCAGAAGCG CGGCCGTCTG
      CGGCCCTGAC AGCCCGCATG TGTTTAGCGG GCGTCTTCGC GCCGGCAGAC
-------------------------------------------------------------------------------
5401  GACCGATGGC TGTGTAGAAG TACTCGCCGA TAGTGGAAAC CGACGCCCCA
      CTGGCTACCG ACACATCTTC ATGAGCGGCT ATCACCTTTG GCTGCGGGGT
-------------------------------------------------------------------------------
5451  GCACTCGTCC GAGGGCAAAG GAATAGAGTA GATGCCGACC GGGATCTATC
      CGTGAGCAGG CTCCCGTTTC CTTATCTCAT CTACGGCTGG CCCTAGATAG
-------------------------------------------------------------------------------
5501  GATAAAATAA AAGATTTTAT TTAGTCTCCA GAAAAAGGGG GGAATGAAAG
      CTATTTTATT TTCTAAAATA AATCAGAGGT CTTTTTCCCC CCTTACTTTC
-------------------------------------------------------------------------------
5551  ACCCCACCTG TAGGTTTGGC AAGCTAGCTT AAGTAACGCC ATTTTGCAAG
      TGGGGTGGAC ATCCAAACCG TTCGATCGAA TTCATTGCGG TAAAACGTTC
-------------------------------------------------------------------------------
5601  GCATGGAAAA ATACATAACT GAGAATAGAG AAGTTCAGAT CAAGGTCAGG
      CGTACCTTTT TATGTATTGA CTCTTATCTC TTCAAGTCTA GTTCCAGTCC
-------------------------------------------------------------------------------
5651  AACAGATGGA ACAGCTGAAT ATGGGCCAAA CAGGATATCT GTGGTAAGCA
      TTGTCTACCT TGTCGACTTA TACCCGGTTT GTCCTATAGA CACCATTCGT
-------------------------------------------------------------------------------
```

```
5701  GTTCCTGCCC CGGCTCAGGG CCAAGAACAG ATGGAACAGC TGAATATGGG
      CAAGGACGGG GCCGAGTCCC GGTTCTTGTC TACCTTGTCG ACTTATACCC
 ----------------------------------------------------------------------------------
5751  CCAAACAGGA TATCTGTGGT AAGCAGTTCC TGCCCCGGCT CAGGGCCAAG
      GGTTTGTCCT ATAGACACCA TTCGTCAAGG ACGGGGCCGA GTCCCGGTTC
 ----------------------------------------------------------------------------------
5801  AACAGATGGT CCCCAGATGC GGTCCAGCCC TCAGCAGTTT CTAGAGAACC
      TTGTCTACCA GGGGTCTACG CCAGGTCGGG AGTCGTCAAA GATCTCTTGG
 ----------------------------------------------------------------------------------
5851  ATCAGATGTT TCCAGGGTGC CCCAAGGACC TGAAATGACC CTGTGCCTTA
      TAGTCTACAA AGGTCCCACG GGGTTCCTGG ACTTTACTGG GACACGGAAT
 ----------------------------------------------------------------------------------
5901  TTTGAACTAA CCAATCAGTT CGCTTCTCGC TTCTGTTCGC GCGCTTCTGC
      AAACTTGATT GGTTAGTCAA GCGAAGAGCG AAGACAAGCG CGCGAAGACG
 ----------------------------------------------------------------------------------
5951  TCCCCGAGCT CAATAAAAGA GCCCACAACC CCTCACTCGG GGCGCCAGTC
      AGGGGCTCGA GTTATTTTCT CGGGTGTTGG GGAGTGAGCC CCGCGGTCAG
 ----------------------------------------------------------------------------------
6001  CTCCGATTGA CTGAGTCGCC CGGGTACCCG TGTATCCAAT AAACCCTCTT
      GAGGCTAACT GACTCAGCGG GCCCATGGGC ACATAGGTTA TTTGGGAGAA
 ----------------------------------------------------------------------------------
6051  GCAGTTGCAT CCGACTTGTG GTCTCGCTGT TCCTTGGGAG GGTCTCCTCT
      CGTCAACGTA GGCTGAACAC CAGAGCGACA AGGAACCCTC CCAGAGGAGA
 ----------------------------------------------------------------------------------
6101  GAGTGATTGA CTACCCGTCA GCGGGGGTCT TTCATTCATG CAGCATGTAT
      CTCACTAACT GATGGGCAGT CGCCCCCAGA AAGTAAGTAC GTCGTACATA
 ----------------------------------------------------------------------------------
6151  CAAAATTAAT TTGGTTTTTT TTCTTAAGTA TTTACATTAA ATGGCCATAG
      GTTTTAATTA AACCAAAAAA AAGAATTCAT AAATGTAATT TACCGGTATC
 ----------------------------------------------------------------------------------
6201  TTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT TGCGTATTGG
      AACGTAATTA CTTAGCCGGT TGCGCGCCCC TCTCCGCCAA ACGCATAACC
 ----------------------------------------------------------------------------------
6251  CGCTCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG TCGTTCGGCT
      GCGAGAAGGC GAAGGAGCGA GTGACTGAGC GACGCGAGCC AGCAAGCCGA
 ----------------------------------------------------------------------------------
6301  GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
      CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC
 ----------------------------------------------------------------------------------
6351  AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG
      TTAGTCCCCT ATTGCGTCCT TTCTTGTACA CTCGTTTTCC GGTCGTTTTC
 ----------------------------------------------------------------------------------
6401  GCCAGGAACC GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG
      CGGTCCTTGG CATTTTTCCG GCGCAACGAC CGCAAAAAGG TATCCGAGGC
 ----------------------------------------------------------------------------------
6451  CCCCCCTGAC GAGCATCACA AAAATCGACG CTCAAGTCAG AGGTGGCGAA
      GGGGGGACTG CTCGTAGTGT TTTTAGCTGC GAGTTCAGTC TCCACCGCTT
 ----------------------------------------------------------------------------------
6501  ACCCGACAGG ACTATAAAGA TACCAGGCGT TTCCCCCTGG AAGCTCCCTC
      TGGGCTGTCC TGATATTTCT ATGGTCCGCA AAGGGGGACC TTCGAGGGAG
 ----------------------------------------------------------------------------------
6551  GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC TGTCCGCCTT
      CACGCGAGAG GACAAGGCTG GGACGGCGAA TGGCCTATGG ACAGGCGGAA
 ----------------------------------------------------------------------------------
6601  TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA TAGCTCACGC TGTAGGTATC
      AGAGGGAAGC CCTTCGCACC GCGAAAGAGT ATCGAGTGCG ACATCCATAG
 ----------------------------------------------------------------------------------
```

```
6651  TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC
      AGTCAAGCCA CATCCAGCAA GCGAGGTTCG ACCCGACACA CGTGCTTGGG
 ----------------------------------------------------------------------------------
6701  CCCGTTCAGC CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC
      GGGCAAGTCG GGCTGGCGAC GCGGAATAGG CCATTGATAG CAGAACTCAG
 ----------------------------------------------------------------------------------
6751  CAACCCGGTA AGACACGACT TATCGCCACT GGCAGCAGCC ACTGGTAACA
      GTTGGGCCAT TCTGTGCTGA ATAGCGGTGA CCGTCGTCGG TGACCATTGT
 ----------------------------------------------------------------------------------
6801  GGATTAGCAG AGCGAGGTAT GTAGGCGGTG CTACAGAGTT CTTGAAGTGG
      CCTAATCGTC TCGCTCCATA CATCCGCCAC GATGTCTCAA GAACTTCACC
 ----------------------------------------------------------------------------------
6851  TGGCCTAACT ACGGCTACAC TAGAAGAACA GTATTTGGTA TCTGCGCTCT
      ACCGGATTGA TGCCGATGTG ATCTTCTTGT CATAAACCAT AGACGCGAGA
 ----------------------------------------------------------------------------------
6901  GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA
      CGACTTCGGT CAATGGAAGC CTTTTTCTCA ACCATCGAGA ACTAGGCCGT
 ----------------------------------------------------------------------------------
6951  AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTTGCAA GCAGCAGATT
      TTGTTTGGTG GCGACCATCG CCACCAAAAA AACAAACGTT CGTCGTCTAA
 ----------------------------------------------------------------------------------
7001  ACGCGCAGAA AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG
      TGCGCGTCTT TTTTTCCTAG AGTTCTTCTA GGAAACTAGA AAAGATGCCC
 ----------------------------------------------------------------------------------
7051  GTCTGACGCT CAGTGGAACG AAAACTCACG TTAAGGGATT TTGGTCATGA
      CAGACTGCGA GTCACCTTGC TTTTGAGTGC AATTCCCTAA AACCAGTACT
 ----------------------------------------------------------------------------------
7101  GATTATCAAA AAGGATCTTC ACCTAGATCC TTTTAAATTA AAAATGAAGT
      CTAATAGTTT TTCCTAGAAG TGGATCTAGG AAAATTTAAT TTTTACTTCA
 ----------------------------------------------------------------------------------
7151  TTGCGGCCGC AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA
      AACGCCGGCG TTTAGTTAGA TTTCATATAT ACTCATTTGA ACCAGACTGT
 ----------------------------------------------------------------------------------
7201  GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT
      CAATGGTTAC GAATTAGTCA CTCCGTGGAT AGAGTCGCTA GACAGATAAA
 ----------------------------------------------------------------------------------
7251  CGTTCATCCA TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG
      GCAAGTAGGT ATCAACGGAC TGAGGGGCAG CACATCTATT GATGCTATGC
 ----------------------------------------------------------------------------------
7301  GGAGGGCTTA CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC
      CCTCCCGAAT GGTAGACCGG GGTCACGACG TTACTATGGC GCTCTGGGTG
 ----------------------------------------------------------------------------------
7351  GCTCACCGGC TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC
      CGAGTGGCCG AGGTCTAAAT AGTCGTTATT TGGTCGGTCG GCCTTCCCGG
 ----------------------------------------------------------------------------------
7401  GAGCGCAGAA GTGGTCCTGC AACTTTATCC GCCTCCATCC AGTCTATTAA
      CTCGCGTCTT CACCAGGACG TTGAAATAGG CGGAGGTAGG TCAGATAATT
 ----------------------------------------------------------------------------------
7451  TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA
      AACAACGGCC CTTCGATCTC ATTCATCAAG CGGTCAATTA TCAAACGCGT
 ----------------------------------------------------------------------------------
7501  ACGTTGTTGC CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTTGGT
      TGCAACAACG GTAACGATGT CCGTAGCACC ACAGTGCGAG CAGCAAACCA
 ----------------------------------------------------------------------------------
7551  ATGGCTTCAT TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC
      TACCGAAGTA AGTCGAGGCC AAGGGTTGCT AGTTCCGCTC AATGTACTAG
 ----------------------------------------------------------------------------------
```

```
7601  CCCCATGTTG TGCAAAAAAG CGGTTAGCTC CTTCGGTCCT CCGATCGTTG
      GGGGTACAAC ACGTTTTTTC GCCAATCGAG GAAGCCAGGA GGCTAGCAAC
-------------------------------------------------------------------------------
7651  TCAGAAGTAA GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG
      AGTCTTCATT CAACCGGCGT CACAATAGTG AGTACCAATA CCGTCGTGAC
-------------------------------------------------------------------------------
7701  CATAATTCTC TTACTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG
      GTATTAAGAG AATGACAGTA CGGTAGGCAT TCTACGAAAA GACACTGACC
-------------------------------------------------------------------------------
7751  TGAGTACTCA ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT
      ACTCATGAGT TGGTTCAGTA AGACTCTTAT CACATACGCC GCTGGCTCAA
-------------------------------------------------------------------------------
7801  GCTCTTGCCC GGCGTCAATA CGGGATAATA CCGCGCCACA TAGCAGAACT
      CGAGAACGGG CCGCAGTTAT GCCCTATTAT GGCGCGGTGT ATCGTCTTGA
-------------------------------------------------------------------------------
7851  TTAAAAGTGC TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG
      AATTTTCACG AGTAGTAACC TTTTGCAAGA AGCCCCGCTT TTGAGAGTTC
-------------------------------------------------------------------------------
7901  GATCTTACCG CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA
      CTAGAATGGC GACAACTCTA GGTCAAGCTA CATTGGGTGA GCACGTGGGT
-------------------------------------------------------------------------------
7951  ACTGATCTTC AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA
      TGACTAGAAG TCGTAGAAAA TGAAAGTGGT CGCAAAGACC CACTCGTTTT
-------------------------------------------------------------------------------
8001  ACAGGAAGGC AAAATGCCGC AAAAAAGGGA ATAAGGGCGA CACGGAAATG
      TGTCCTTCCG TTTTACGGCG TTTTTTCCCT TATTCCCGCT GTGCCTTTAC
-------------------------------------------------------------------------------
8051  TTGAATACTC ATACTCTTCC TTTTTCAATA TTATTGAAGC ATTTATCAGG
      AACTTATGAG TATGAGAAGG AAAAAGTTAT AATAACTTCG TAAATAGTCC
-------------------------------------------------------------------------------
8101  GTTATTGTCT CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA
      CAATAACAGA GTACTCGCCT ATGTATAAAC TTACATAAAT CTTTTTATTT
-------------------------------------------------------------------------------
8151  CAAATAGGGG TTCCGCGCAC ATTTC
      GTTTATCCCC AAGGCGCGTG TAAAG
-------------------------------------------------------------------------------
```

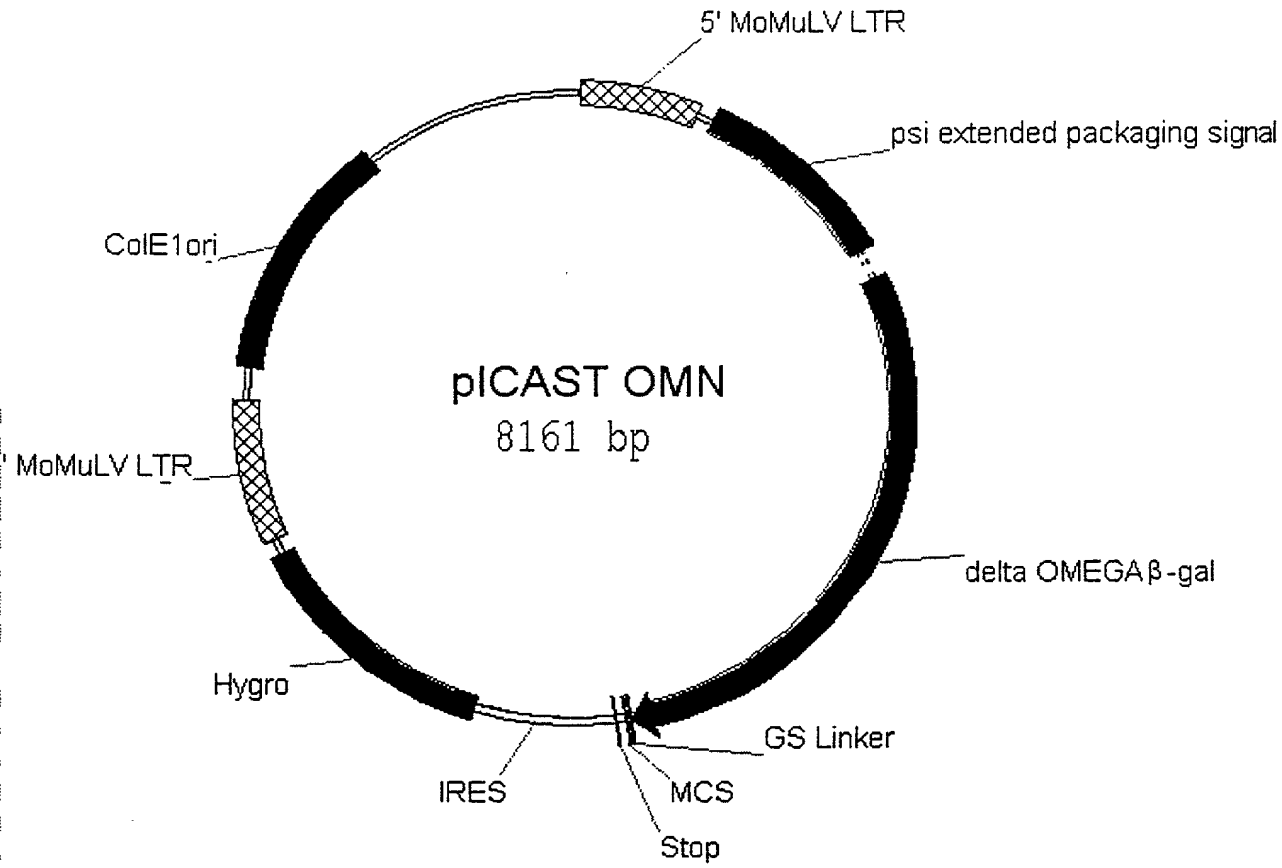
5' MoMuLV LTR
psi extended packaging signal
ColE1ori
pICAST OMN
8161 bp
3' MoMuLV LTR
delta OMEGA β-gal
Hygro
GS Linker
IRES
MCS
Stop

Figure 13A

```
  1  CTGCAGCCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG
     GACGTCGGAC TTATACCCGG TTTGTCCTAT AGACACCATT CGTCAAGGAC
---------------------------------------------------------------------------
 51  CCCCGGCTCA GGGCCAAGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA
     GGGGCCGAGT CCCGGTTCTT GTCTACCTTG TCGACTTATA CCCGGTTTGT
---------------------------------------------------------------------------
101  GGATATCTGT GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT
     CCTATAGACA CCATTCGTCA AGGACGGGGC CGAGTCCCGG TTCTTGTCTA
---------------------------------------------------------------------------
151  GGTCCCCAGA TGCGGTCCAG CCCTCAGCAG TTTCTAGAGA ACCATCAGAT
     CCAGGGGTCT ACGCCAGGTC GGGAGTCGTC AAAGATCTCT TGGTAGTCTA
---------------------------------------------------------------------------
201  GTTTCCAGGG TGCCCCAAGG ACCTGAAATG ACCCTGTGCC TTATTTGAAC
     CAAAGGTCCC ACGGGGTTCC TGGACTTTAC TGGGACACGG AATAAACTTG
---------------------------------------------------------------------------
251  TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC TGCTCCCCGA
     ATTGGTTAGT CAAGCGAAGA GCGAAGACAA GCGCGCGAAG ACGAGGGGCT
---------------------------------------------------------------------------
301  GCTCAATAAA AGAGCCCACA ACCCCTCACT CGGGGCGCCA GTCCTCCGAT
     CGAGTTATTT TCTCGGGTGT TGGGGAGTGA GCCCCGCGGT CAGGAGGCTA
---------------------------------------------------------------------------
351  TGACTGAGTC GCCCGGGTAC CCGTGTATCC AATAAACCCT CTTGCAGTTG
     ACTGACTCAG CGGGCCCATG GGCACATAGG TTATTTGGGA GAACGTCAAC
---------------------------------------------------------------------------
401  CATCCGACTT GTGGTCTCGC TGTTCCTTGG GAGGGTCTCC TCTGAGTGAT
     GTAGGCTGAA CACCAGAGCG ACAAGGAACC CTCCCAGAGG AGACTCACTA
---------------------------------------------------------------------------
451  TGACTACCCG TCAGCGGGGG TCTTTCATTT GGGGGCTCGT CCGGGATCGG
     ACTGATGGGC AGTCGCCCCC AGAAAGTAAA CCCCCGAGCA GGCCCTAGCC
---------------------------------------------------------------------------
501  GAGACCCCTG CCCAGGGACC ACCGACCCAC CACCGGGAGG CAAGCTGGCC
     CTCTGGGGAC GGGTCCCTGG TGGCTGGGTG GTGGCCCTCC GTTCGACCGG
---------------------------------------------------------------------------
551  AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG ACTGATTTTA
     TCGTTGAATA GACACAGACA GGCTAACAGA TCACAGATAC TGACTAAAAT
---------------------------------------------------------------------------
601  TGCGCCTGCG TCGGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC
     ACGCGGACGC AGCCATGATC AATCGATTGA TCGAGACATA GACCGCCTGG
---------------------------------------------------------------------------
651  CGTGGTGGAA CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG
     GCACCACCTT GACTGCTCAA GACTTGTGGG CCGGCGTTGG GACCCTCTGC
---------------------------------------------------------------------------
701  TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG CCCGACCTGA GGAAGGGAGT
     AGGGTCCCTG AAACCCCCGG CAAAAACACC GGGCTGGACT CCTTCCCTCA
---------------------------------------------------------------------------
751  CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT AGGAGACGAG
     GCTACACCTT AGGCTGGGGC AGTCCTATAC ACCAAGACCA TCCTCTGCTC
---------------------------------------------------------------------------
801  AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA
     TTGGATTTTG TCAAGGGCGG AGGCAGACTT AAAAACGAAA GCCAAACCTT
---------------------------------------------------------------------------
851  CCGAAGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT
     GGCTTCGGCG CGCAGAACAG ACGACGTCGT AGCAAGACAC AACAGAGACA
---------------------------------------------------------------------------
901  CTGACTGTGT TTCTGTATTT GTCTGAAAAT TAGGGCCAGA CTGTTACCAC
     GACTGACACA AAGACATAAA CAGACTTTTA ATCCCGGTCT GACAATGGTG
---------------------------------------------------------------------------
```

FIGURE 13B

```
 951  TCCCTTAAGT TTGACCTTAG GTAACTGGAA AGATGTCGAG CGGCTCGCTC
      AGGGAATTCA AACTGGAATC CATTGACCTT TCTACAGCTC GCCGAGCGAG
-------------------------------------------------------------------------------
1001  ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
      TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
-------------------------------------------------------------------------------
1051  GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
      CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
-------------------------------------------------------------------------------
1101  CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
      GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
-------------------------------------------------------------------------------
1151  ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
      TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
-------------------------------------------------------------------------------
1201  TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
      AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
-------------------------------------------------------------------------------
1251  TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
      AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
-------------------------------------------------------------------------------
1301  CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
      GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
-------------------------------------------------------------------------------
1351  GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAACACCA
      CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTGTGGT
-------------------------------------------------------------------------------
1401  TGCACCATCA TCATCATCAC GTCGACGAAC AGAAACTCAT TTCCGAAGAA
      ACGTGGTAGT AGTAGTAGTG CAGCTGCTTG TCTTTGAGTA AAGGCTTCTT
-------------------------------------------------------------------------------
1451  GACCTACTCG AGATGGGCGT GATTACGGAT TCACTGGCCG TCGTTTTACA
      CTGGATGAGC TCTACCCGCA CTAATGCCTA AGTGACCGGC AGCAAAATGT
-------------------------------------------------------------------------------
1501  ACGTCGTGAC TGGGAAAACC CTGGCGTTAC CCAACTTAAT CGCCTTGCAG
      TGCAGCACTG ACCCTTTTGG GACCGCAATG GGTTGAATTA GCGGAACGTC
-------------------------------------------------------------------------------
1551  CACATCCCCC TTTCGCCAGC TGGCGTAATA GCGAAGAGGC CCGCACCGAT
      GTGTAGGGGG AAAGCGGTCG ACCGCATTAT CGCTTCTCCG GGCGTGGCTA
-------------------------------------------------------------------------------
1601  CGCCCTTCCC AACAGTTACG CAGCCTGAAT GGCGAATGGC GCTTTGCCTG
      GCGGGAAGGG TTGTCAATGC GTCGGACTTA CCGCTTACCG CGAAACGGAC
-------------------------------------------------------------------------------
1651  GTTTCCGGCA CCAGAAGCGG TGCCGGAAAG CTGGCTGGAG TGCGATCTTC
      CAAAGGCCGT GGTCTTCGCC ACGGCCTTTC GACCGACCTC ACGCTAGAAG
-------------------------------------------------------------------------------
1701  CTGAGGCCGA TACTGTCGTC GTCCCCTCAA ACTGGCAGAT GCACGGTTAC
      GACTCCGGCT ATGACAGCAG CAGGGGAGTT TGACCGTCTA CGTGCCAATG
-------------------------------------------------------------------------------
1751  GATGCGCCCA TCTACACCAA CGTGACCTAT CCCATTACGG TCAATCCGCC
      CTACGCGGGT AGATGTGGTT GCACTGGATA GGGTAATGCC AGTTAGGCGG
-------------------------------------------------------------------------------
1801  GTTTGTTCCC ACGGAGAATC CGACGGGTTG TTACTCGCTC ACATTTAATG
      CAAACAAGGG TGCCTCTTAG GCTGCCCAAC AATGAGCGAG TGTAAATTAC
-------------------------------------------------------------------------------
1851  TTGATGAAAG CTGGCTACAG GAAGGCCAGA CGCGAATTAT TTTTGATGGC
      AACTACTTTC GACCGATGTC CTTCCGGTCT GCGCTTAATA AAAACTACCG
-------------------------------------------------------------------------------
```

```
1901  GTTAACTCGG CGTTTCATCT GTGGTGCAAC GGGCGCTGGG TCGGTTACGG
      CAATTGAGCC GCAAAGTAGA CACCACGTTG CCCGCGACCC AGCCAATGCC
-------------------------------------------------------------------------------
1951  CCAGGACAGT CGTTTGCCGT CTGAATTTGA CCTGAGCGCA TTTTTACGCG
      GGTCCTGTCA GCAAACGGCA GACTTAAACT GGACTCGCGT AAAAATGCGC
-------------------------------------------------------------------------------
2001  CCGGAGAAAA CCGCCTCGCG GTGATGGTGC TGCGCTGGAG TGACGGCAGT
      GGCCTCTTTT GGCGGAGCGC CACTACCACG ACGCGACCTC ACTGCCGTCA
-------------------------------------------------------------------------------
2051  TATCTGGAAG ATCAGGATAT GTGGCGGATG AGCGGCATTT TCCGTGACGT
      ATAGACCTTC TAGTCCTATA CACCGCCTAC TCGCCGTAAA AGGCACTGCA
-------------------------------------------------------------------------------
2101  CTCGTTGCTG CATAAACCGA CTACACAAAT CAGCGATTTC CATGTTGCCA
      GAGCAACGAC GTATTTGGCT GATGTGTTTA GTCGCTAAAG GTACAACGGT
-------------------------------------------------------------------------------
2151  CTCGCTTTAA TGATGATTTC AGCCGCGCTG TACTGGAGGC TGAAGTTCAG
      GAGCGAAATT ACTACTAAAG TCGGCGCGAC ATGACCTCCG ACTTCAAGTC
-------------------------------------------------------------------------------
2201  ATGTGCGGCG AGTTGCGTGA CTACCTACGG GTAACAGTTT CTTTATGGCA
      TACACGCCGC TCAACGCACT GATGGATGCC CATTGTCAAA GAAATACCGT
-------------------------------------------------------------------------------
2251  GGGTGAAACG CAGGTCGCCA GCGGCACCGC GCCTTTCGGC GGTGAAATTA
      CCCACTTTGC GTCCAGCGGT CGCCGTGGCG CGGAAAGCCG CCACTTTAAT
-------------------------------------------------------------------------------
2301  TCGATGAGCG TGGTGGTTAT GCCGATCGCG TCACACTACG TCTGAACGTC
      AGCTACTCGC ACCACCAATA CGGCTAGCGC AGTGTGATGC AGACTTGCAG
-------------------------------------------------------------------------------
2351  GAAAACCCGA AACTGTGGAG CGCCGAAATC CCGAATCTCT ATCGTGCGGT
      CTTTTGGGCT TTGACACCTC GCGGCTTTAG GGCTTAGAGA TAGCACGCCA
-------------------------------------------------------------------------------
2401  GGTTGAACTG CACACCGCCG ACGGCACGCT GATTGAAGCA GAAGCCTGCG
      CCAACTTGAC GTGTGGCGGC TGCCGTGCGA CTAACTTCGT CTTCGGACGC
-------------------------------------------------------------------------------
2451  ATGTCGGTTT CCGCGAGGTG CGGATTGAAA ATGGTCTGCT GCTGCTGAAC
      TACAGCCAAA GGCGCTCCAC GCCTAACTTT TACCAGACGA CGACGACTTG
-------------------------------------------------------------------------------
2501  GGCAAGCCGT TGCTGATTCG AGGCGTTAAC CGTCACGAGC ATCATCCTCT
      CCGTTCGGCA ACGACTAAGC TCCGCAATTG GCAGTGCTCG TAGTAGGAGA
-------------------------------------------------------------------------------
2551  GCATGGTCAG GTCATGGATG AGCAGACGAT GGTGCAGGAT ATCCTGCTGA
      CGTACCAGTC CAGTACCTAC TCGTCTGCTA CCACGTCCTA TAGGACGACT
-------------------------------------------------------------------------------
2601  TGAAGCAGAA CAACTTTAAC GCCGTGCGCT GTTCGCATTA TCCGAACCAT
      ACTTCGTCTT GTTGAAATTG CGGCACGCGA CAAGCGTAAT AGGCTTGGTA
-------------------------------------------------------------------------------
2651  CCGCTGTGGT ACACGCTGTG CGACCGCTAC GGCCTGTATG TGGTGGATGA
      GGCGACACCA TGTGCGACAC GCTGGCGATG CCGGACATAC ACCACCTACT
-------------------------------------------------------------------------------
2701  AGCCAATATT GAAACCCACG GCATGGTGCC AATGAATCGT CTGACCGATG
      TCGGTTATAA CTTTGGGTGC CGTACCACGG TTACTTAGCA GACTGGCTAC
-------------------------------------------------------------------------------
2751  ATCCGCGCTG GCTACCGGCG ATGAGCGAAC GCGTAACGCG AATGGTGCAG
      TAGGCGCGAC CGATGGCCGC TACTCGCTTG CGCATTGCGC TTACCACGTC
-------------------------------------------------------------------------------
2801  CGCGATCGTA ATCACCCGAG TGTGATCATC TGGTCGCTGG GGAATGAATC
      GCGCTAGCAT TAGTGGGCTC ACACTAGTAG ACCAGCGACC CCTTACTTAG
-------------------------------------------------------------------------------
```

```
2851  AGGCCACGGC GCTAATCACG ACGCGCTGTA TCGCTGGATC AAATCTGTCG
      TCCGGTGCCG CGATTAGTGC TGCGCGACAT AGCGACCTAG TTTAGACAGC
-------------------------------------------------------------------------------
2901  ATCCTTCCCG CCCGGTGCAG TATGAAGGCG GCGGAGCCGA CACCACGGCC
      TAGGAAGGGC GGGCCACGTC ATACTTCCGC CGCCTCGGCT GTGGTGCCGG
-------------------------------------------------------------------------------
2951  ACCGATATTA TTTGCCCGAT GTACGCGCGC GTGGATGAAG ACCAGCCCTT
      TGGCTATAAT AAACGGGCTA CATGCGCGCG CACCTACTTC TGGTCGGGAA
-------------------------------------------------------------------------------
3001  CCCGGCTGTG CCGAAATGGT CCATCAAAAA ATGGCTTTCG CTACCTGGAG
      GGGCCGACAC GGCTTTACCA GGTAGTTTTT TACCGAAAGC GATGGACCTC
-------------------------------------------------------------------------------
3051  AGACGCGCCC GCTGATCCTT TGCGAATACG CCCACGCGAT GGGTAACAGT
      TCTGCGCGGG CGACTAGGAA ACGCTTATGC GGGTGCGCTA CCCATTGTCA
-------------------------------------------------------------------------------
3101  CTTGGCGGTT TCGCTAAATA CTGGCAGGCG TTTCGTCAGT ATCCCCGTTT
      GAACCGCCAA AGCGATTTAT GACCGTCCGC AAAGCAGTCA TAGGGGCAAA
-------------------------------------------------------------------------------
3151  ACAGGGCGGC TTCGTCTGGG ACTGGGTGGA TCAGTCGCTG ATTAAATATG
      TGTCCCGCCG AAGCAGACCC TGACCCACCT AGTCAGCGAC TAATTTATAC
-------------------------------------------------------------------------------
3201  ATGAAAACGG CAACCCGTGG TCGGCTTACG GCGGTGATTT TGGCGATACG
      TACTTTTGCC GTTGGGCACC AGCCGAATGC CGCCACTAAA ACCGCTATGC
-------------------------------------------------------------------------------
3251  CCGAACGATC GCCAGTTCTG TATGAACGGT CTGGTCTTTG CCGACCGCAC
      GGCTTGCTAG CGGTCAAGAC ATACTTGCCA GACCAGAAAC GGCTGGCGTG
-------------------------------------------------------------------------------
3301  GCCGCATCCA GCGCTGACGG AAGCAAAACA CCAGCAGCAG TTTTTCCAGT
      CGGCGTAGGT CGCGACTGCC TTCGTTTTGT GGTCGTCGTC AAAAAGGTCA
-------------------------------------------------------------------------------
3351  TCCGTTTATC CGGGCAAACC ATCGAAGTGA CCAGCGAATA CCTGTTCCGT
      AGGCAAATAG GCCCGTTTGG TAGCTTCACT GGTCGCTTAT GGACAAGGCA
-------------------------------------------------------------------------------
3401  CATAGCGATA ACGAGCTCCT GCACTGGATG GTGGCGCTGG ATGGTAAGCC
      GTATCGCTAT TGCTCGAGGA CGTGACCTAC CACCGCGACC TACCATTCGG
-------------------------------------------------------------------------------
3451  GCTGGCAAGC GGTGAAGTGC CTCTGGATGT CGCTCCACAA GGTAAACAGT
      CGACCGTTCG CCACTTCACG GAGACCTACA GCGAGGTGTT CCATTTGTCA
-------------------------------------------------------------------------------
3501  TGATTGAACT GCCTGAACTA CCGCAGCCGG AGAGCGCCGG GCAACTCTGG
      ACTAACTTGA CGGACTTGAT GGCGTCGGCC TCTCGCGGCC CGTTGAGACC
-------------------------------------------------------------------------------
3551  CTCACAGTAC GCGTAGTGCA ACCGAACGCG ACCGCATGGT CAGAAGCCGG
      GAGTGTCATG CGCATCACGT TGGCTTGCGC TGGCGTACCA GTCTTCGGCC
-------------------------------------------------------------------------------
3601  GCACATCAGC GCCTGGCAGC AGTGGCGTCT GGCGGAAAAC CTCAGTGTGA
      CGTGTAGTCG CGGACCGTCG TCACCGCAGA CCGCCTTTTG GAGTCACACT
-------------------------------------------------------------------------------
3651  CGCTCCCCGC CGCGTCCCAC GCCATCCCGC ATCTGACCAC CAGCGAAATG
      GCGAGGGGCG GCGCAGGGTG CGGTAGGGCG TAGACTGGTG GTCGCTTTAC
-------------------------------------------------------------------------------
3701  GATTTTTGCA TCGAGCTGGG TAATAAGCGT TGGCAATTTA ACCGCCAGTC
      CTAAAAACGT AGCTCGACCC ATTATTCGCA ACCGTTAAAT TGGCGGTCAG
-------------------------------------------------------------------------------
3751  AGGCTTTCTT TCACAGATGT GGATTGGCGA TAAAAAACAA CTGCTGACGC
      TCCGAAAGAA AGTGTCTACA CCTAACCGCT ATTTTTTGTT GACGACTGCG
-------------------------------------------------------------------------------
```

```
3801  CGCTGCGCGA TCAGTTCACC CGTGTCGATA GATCTGGAGG TGGTGGCAGC
      GCGACGCGCT AGTCAAGTGG GCACAGCTAT CTAGACCTCC ACCACCGTCG
-------------------------------------------------------------------------------
3851  AGGCCTTGGC GCGCCGGATC CTTAATTAAC AATTGACCGG TAATAATAGG
      TCCGGAACCG CGCGGCCTAG GAATTAATTG TTAACTGGCC ATTATTATCC
-------------------------------------------------------------------------------
3901  TAGATAAGTG ACTGATTAGA TGCATTTCGA CTAGATCCCT CGACCAATTC
      ATCTATTCAC TGACTAATCT ACGTAAAGCT GATCTAGGGA GCTGGTTAAG
-------------------------------------------------------------------------------
3951  CGGTTATTTT CCACCATATT GCCGTCTTTT GGCAATGTGA GGGCCCGGAA
      GCCAATAAAA GGTGGTATAA CGGCAGAAAA CCGTTACACT CCCGGGCCTT
-------------------------------------------------------------------------------
4001  ACCTGGCCCT GTCTTCTTGA CGAGCATTCC TAGGGGTCTT TCCCCTCTCG
      TGGACCGGGA CAGAAGAACT GCTCGTAAGG ATCCCCAGAA AGGGGAGAGC
-------------------------------------------------------------------------------
4051  CCAAAGGAAT GCAAGGTCTG TTGAATGTCG TGAAGGAAGC AGTTCCTCTG
      GGTTTCCTTA CGTTCCAGAC AACTTACAGC ACTTCCTTCG TCAAGGAGAC
-------------------------------------------------------------------------------
4101  GAAGCTTCTT GAAGACAAAC AACGTCTGTA GCGACCCTTT GCAGGCAGCG
      CTTCGAAGAA CTTCTGTTTG TTGCAGACAT CGCTGGGAAA CGTCCGTCGC
-------------------------------------------------------------------------------
4151  GAACCCCCCA CCTGGCGACA GGTGCCTCTG CGGCCAAAAG CCACGTGTAT
      CTTGGGGGGT GGACCGCTGT CCACGGAGAC GCCGGTTTTC GGTGCACATA
-------------------------------------------------------------------------------
4201  AAGATACACC TGCAAAGGCG GCACAACCCC AGTGCCACGT TGTGAGTTGG
      TTCTATGTGG ACGTTTCCGC CGTGTTGGGG TCACGGTGCA ACACTCAACC
-------------------------------------------------------------------------------
4251  ATAGTTGTGG AAAGAGTCAA ATGGCTCTCC TCAAGCGTAT TCAACAAGGG
      TATCAACACC TTTCTCAGTT TACCGAGAGG AGTTCGCATA AGTTGTTCCC
-------------------------------------------------------------------------------
4301  GCTGAAGGAT GCCCAGAAGG TACCCCATTG TATGGGATCT GATCTGGGGC
      CGACTTCCTA CGGGTCTTCC ATGGGGTAAC ATACCCTAGA CTAGACCCCG
-------------------------------------------------------------------------------
4351  CTCGGTGCAC ATGCTTTACA TGTGTTTAGT CGAGGTTAAA AAACGTCTAG
      GAGCCACGTG TACGAAATGT ACACAAATCA GCTCCAATTT TTTGCAGATC
-------------------------------------------------------------------------------
4401  GCCCCCCGAA CCACGGGGAC GTGGTTTTCC TTTGAAAAAC ACGATGATAA
      CGGGGGGCTT GGTGCCCCTG CACCAAAAGG AAACTTTTTG TGCTACTATT
-------------------------------------------------------------------------------
4451  TACCATGAAA AAGCCTGAAC TCACCGCGAC GTCTGTCGAG AAGTTTCTGA
      ATGGTACTTT TTCGGACTTG AGTGGCGCTG CAGACAGCTC TTCAAAGACT
-------------------------------------------------------------------------------
4501  TCGAAAAGTT CGACAGCGTC TCCGACCTGA TGCAGCTCTC GGAGGGCGAA
      AGCTTTTCAA GCTGTCGCAG AGGCTGGACT ACGTCGAGAG CCTCCCGCTT
-------------------------------------------------------------------------------
4551  GAATCTCGTG CTTTCAGCTT CGATGTAGGA GGGCGTGGAT ATGTCCTGCG
      CTTAGAGCAC GAAAGTCGAA GCTACATCCT CCCGCACCTA TACAGGACGC
-------------------------------------------------------------------------------
4601  GGTAAATAGC TGCGCCGATG GTTTCTACAA AGATCGTTAT GTTTATCGGC
      CCATTTATCG ACGCGGCTAC CAAAGATGTT TCTAGCAATA CAAATAGCCG
-------------------------------------------------------------------------------
4651  ACTTTGCATC GGCCGCGCTC CCGATTCCGG AAGTGCTTGA CATTGGGGAA
      TGAAACGTAG CCGGCGCGAG GGCTAAGGCC TTCACGAACT GTAACCCCTT
-------------------------------------------------------------------------------
4701  TTTAGCGAGA GCCTGACCTA TTGCATCTCC CGCCGTGCAC AGGGTGTCAC
      AAATCGCTCT CGGACTGGAT AACGTAGAGG GCGGCACGTG TCCCACAGTG
-------------------------------------------------------------------------------
```

```
4751  GTTGCAAGAC CTGCCTGAAA CCGAACTGCC CGCTGTTCTG CAGCCGGTCG
      CAACGTTCTG GACGGACTTT GGCTTGACGG GCGACAAGAC GTCGGCCAGC
 ----------------------------------------------------------------------------------------
4801  CGGAGGCCAT GGATGCGATC GCTGCGGCCG ATCTTAGCCA GACGAGCGGG
      GCCTCCGGTA CCTACGCTAG CGACGCCGGC TAGAATCGGT CTGCTCGCCC
 ----------------------------------------------------------------------------------------
4851  TTCGGCCCAT TCGGACCGCA AGGAATCGGT CAATACACTA CATGGCGTGA
      AAGCCGGGTA AGCCTGGCGT TCCTTAGCCA GTTATGTGAT GTACCGCACT
 ----------------------------------------------------------------------------------------
4901  TTTCATATGC GCGATTGCTG ATCCCCATGT GTATCACTGG CAAACTGTGA
      AAAGTATACG CGCTAACGAC TAGGGGTACA CATAGTGACC GTTTGACACT
 ----------------------------------------------------------------------------------------
4951  TGGACGACAC CGTCAGTGCG TCCGTCGCGC AGGCTCTCGA TGAGCTGATG
      ACCTGCTGTG GCAGTCACGC AGGCAGCGCG TCCGAGAGCT ACTCGACTAC
 ----------------------------------------------------------------------------------------
5001  CTTTGGGCCG AGGACTGCCC CGAAGTCCGG CACCTCGTGC ACGCGGATTT
      GAAACCCGGC TCCTGACGGG GCTTCAGGCC GTGGAGCACG TGCGCCTAAA
 ----------------------------------------------------------------------------------------
5051  CGGCTCCAAC AATGTCCTGA CGGACAATGG CCGCATAACA GCGGTCATTG
      GCCGAGGTTG TTACAGGACT GCCTGTTACC GGCGTATTGT CGCCAGTAAC
 ----------------------------------------------------------------------------------------
5101  ACTGGAGCGA GGCGATGTTC GGGGATTCCC AATACGAGGT CGCCAACATC
      TGACCTCGCT CCGCTACAAG CCCCTAAGGG TTATGCTCCA GCGGTTGTAG
 ----------------------------------------------------------------------------------------
5151  TTCTTCTGGA GGCCGTGGTT GGCTTGTATG GAGCAGCAGA CGCGCTACTT
      AAGAAGACCT CCGGCACCAA CCGAACATAC CTCGTCGTCT GCGCGATGAA
 ----------------------------------------------------------------------------------------
5201  CGAGCGGAGG CATCCGGAGC TTGCAGGATC GCCGCGGCTC CGGGCGTATA
      GCTCGCCTCC GTAGGCCTCG AACGTCCTAG CGGCGCCGAG GCCCGCATAT
 ----------------------------------------------------------------------------------------
5251  TGCTCCGCAT TGGTCTTGAC CAACTCTATC AGAGCTTGGT TGACGGCAAT
      ACGAGGCGTA ACCAGAACTG GTTGAGATAG TCTCGAACCA ACTGCCGTTA
 ----------------------------------------------------------------------------------------
5301  TTCGATGATG CAGCTTGGGC GCAGGGTCGA TGCGACGCAA TCGTCCGATC
      AAGCTACTAC GTCGAACCCG CGTCCCAGCT ACGCTGCGTT AGCAGGCTAG
 ----------------------------------------------------------------------------------------
5351  CGGAGCCGGG ACTGTCGGGC GTACACAAAT CGCCCGCAGA AGCGCGGCCG
      GCCTCGGCCC TGACAGCCCG CATGTGTTTA GCGGGCGTCT TCGCGCCGGC
 ----------------------------------------------------------------------------------------
5401  TCTGGACCGA TGGCTGTGTA GAAGTACTCG CCGATAGTGG AAACCGACGC
      AGACCTGGCT ACCGACACAT CTTCATGAGC GGCTATCACC TTTGGCTGCG
 ----------------------------------------------------------------------------------------
5451  CCCAGCACTC GTCCGAGGGC AAAGGAATAG AGTAGATGCC GACCGGGATC
      GGGTCGTGAG CAGGCTCCCG TTTCCTTATC TCATCTACGG CTGGCCCTAG
 ----------------------------------------------------------------------------------------
5501  TATCGATAAA ATAAAAGATT TTATTTAGTC TCCAGAAAAA GGGGGGAATG
      ATAGCTATTT TATTTTCTAA AATAAATCAG AGGTCTTTTT CCCCCCTTAC
 ----------------------------------------------------------------------------------------
5551  AAAGACCCCA CCTGTAGGTT TGGCAAGCTA GCTTAAGTAA CGCCATTTTG
      TTTCTGGGGT GGACATCCAA ACCGTTCGAT CGAATTCATT GCGGTAAAAC
 ----------------------------------------------------------------------------------------
5601  CAAGGCATGG AAAAATACAT AACTGAGAAT AGAGAAGTTC AGATCAAGGT
      GTTCCGTACC TTTTTATGTA TTGACTCTTA TCTCTTCAAG TCTAGTTCCA
 ----------------------------------------------------------------------------------------
5651  CAGGAACAGA TGGAACAGCT GAATATGGGC CAAACAGGAT ATCTGTGGTA
      GTCCTTGTCT ACCTTGTCGA CTTATACCCG GTTTGTCCTA TAGACACCAT
 ----------------------------------------------------------------------------------------
```

```
5701  AGCAGTTCCT GCCCCGGCTC AGGGCCAAGA ACAGATGGAA CAGCTGAATA
      TCGTCAAGGA CGGGGCCGAG TCCCGGTTCT TGTCTACCTT GTCGACTTAT
-------------------------------------------------------------------------------
5751  TGGGCCAAAC AGGATATCTG TGGTAAGCAG TTCCTGCCCC GGCTCAGGGC
      ACCCGGTTTG TCCTATAGAC ACCATTCGTC AAGGACGGGG CCGAGTCCCG
-------------------------------------------------------------------------------
5801  CAAGAACAGA TGGTCCCCAG ATGCGGTCCA GCCCTCAGCA GTTTCTAGAG
      GTTCTTGTCT ACCAGGGGTC TACGCCAGGT CGGGAGTCGT CAAAGATCTC
-------------------------------------------------------------------------------
5851  AACCATCAGA TGTTTCCAGG GTGCCCCAAG GACCTGAAAT GACCCTGTGC
      TTGGTAGTCT ACAAAGGTCC CACGGGGTTC CTGGACTTTA CTGGGACACG
-------------------------------------------------------------------------------
5901  CTTATTTGAA CTAACCAATC AGTTCGCTTC TCGCTTCTGT TCGCGCGCTT
      GAATAAACTT GATTGGTTAG TCAAGCGAAG AGCGAAGACA AGCGCGCGAA
-------------------------------------------------------------------------------
5951  CTGCTCCCCG AGCTCAATAA AAGAGCCCAC AACCCCTCAC TCGGGGCGCC
      GACGAGGGGC TCGAGTTATT TTCTCGGGTG TTGGGGAGTG AGCCCCGCGG
-------------------------------------------------------------------------------
6001  AGTCCTCCGA TTGACTGAGT CGCCCGGGTA CCCGTGTATC CAATAAACCC
      TCAGGAGGCT AACTGACTCA GCGGGCCCAT GGGCACATAG GTTATTTGGG
-------------------------------------------------------------------------------
6051  TCTTGCAGTT GCATCCGACT TGTGGTCTCG CTGTTCCTTG GGAGGGTCTC
      AGAACGTCAA CGTAGGCTGA ACACCAGAGC GACAAGGAAC CCTCCCAGAG
-------------------------------------------------------------------------------
6101  CTCTGAGTGA TTGACTACCC GTCAGCGGGG GTCTTTCATT CATGCAGCAT
      GAGACTCACT AACTGATGGG CAGTCGCCCC CAGAAAGTAA GTACGTCGTA
-------------------------------------------------------------------------------
6151  GTATCAAAAT TAATTTGGTT TTTTTTCTTA AGTATTTACA TTAAATGGCC
      CATAGTTTTA ATTAAACCAA AAAAAAGAAT TCATAAATGT AATTTACCGG
-------------------------------------------------------------------------------
6201  ATAGTTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA
      TATCAACGTA ATTACTTAGC CGGTTGCGCG CCCCTCTCCG CCAAACGCAT
-------------------------------------------------------------------------------
6251  TTGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC
      AACCGCGAGA AGGCGAAGGA GCGAGTGACT GAGCGACGCG AGCCAGCAAG
-------------------------------------------------------------------------------
6301  GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC
      CCGACGCCGC TCGCCATAGT CGAGTGAGTT TCCGCCATTA TGCCAATAGG
-------------------------------------------------------------------------------
6351  ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA
      TGTCTTAGTC CCCTATTGCG TCCTTTCTTG TACACTCGTT TTCCGGTCGT
-------------------------------------------------------------------------------
6401  AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC
      TTTCCGGTCC TTGGCATTTT TCCGGCGCAA CGACCGCAAA AAGGTATCCG
-------------------------------------------------------------------------------
6451  TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG
      AGGCGGGGGG ACTGCTCGTA GTGTTTTTAG CTGCGAGTTC AGTCTCCACC
-------------------------------------------------------------------------------
6501  CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC
      GCTTTGGGCT GTCCTGATAT TTCTATGGTC CGCAAAGGGG GACCTTCGAG
-------------------------------------------------------------------------------
6551  CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG
      GGAGCACGCG AGAGGACAAG GCTGGGACGG CGAATGGCCT ATGGACAGGC
-------------------------------------------------------------------------------
6601  CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG
      GGAAAGAGGG AAGCCCTTCG CACCGCGAAA GAGTATCGAG TGCGACATCC
-------------------------------------------------------------------------------
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6651  TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA
      ATAGAGTCAA GCCACATCCA GCAAGCGAGG TTCGACCCGA CACACGTGCT
-------------------------------------------------------------------------------
6701  ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG
      TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG ATAGCAGAAC
-------------------------------------------------------------------------------
6751  AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT
      TCAGGTTGGG CCATTCTGTG CTGAATAGCG GTGACCGTCG TCGGTGACCA
-------------------------------------------------------------------------------
6801  AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA
      TTGTCCTAAT CGTCTCGCTC CATACATCCG CCACGATGTC TCAAGAACTT
-------------------------------------------------------------------------------
6851  GTGGTGGCCT AACTACGGCT ACACTAGAAG AACAGTATTT GGTATCTGCG
      CACCACCGGA TTGATGCCGA TGTGATCTTC TTGTCATAAA CCATAGACGC
-------------------------------------------------------------------------------
6901  CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC
      GAGACGACTT CGGTCAATGG AAGCCTTTTT CTCAACCATC GAGAACTAGG
-------------------------------------------------------------------------------
6951  GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA
      CCGTTTGTTT GGTGGCGACC ATCGCCACCA AAAAAACAAA CGTTCGTCGT
-------------------------------------------------------------------------------
7001  GATTACGCGC AGAAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA
      CTAATGCGCG TCTTTTTTTC CTAGAGTTCT TCTAGGAAAC TAGAAAAGAT
-------------------------------------------------------------------------------
7051  CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC
      GCCCCAGACT GCGAGTCACC TTGCTTTTGA GTGCAATTCC CTAAAACCAG
-------------------------------------------------------------------------------
7101  ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTGC GGCCGCAAAT
      TACTCTAATA GTTTTTCCTA GAAGTGGATC TAGGAAAACG CCGGCGTTTA
-------------------------------------------------------------------------------
7151  CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA CCAATGCTTA
      GTTAGATTTC ATATATACTC ATTTGAACCA GACTGTCAAT GGTTACGAAT
-------------------------------------------------------------------------------
7201  ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT
      TAGTCACTCC GTGGATAGAG TCGCTAGACA GATAAAGCAA GTAGGTATCA
-------------------------------------------------------------------------------
7251  TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT
      ACGGACTGAG GGGCAGCACA TCTATTGATG CTATGCCCTC CCGAATGGTA
-------------------------------------------------------------------------------
7301  CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC ACCGGCTCCA
      GACCGGGGTC ACGACGTTAC TATGGCGCTC TGGGTGCGAG TGGCCGAGGT
-------------------------------------------------------------------------------
7351  GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC GCAGAAGTGG
      CTAAATAGTC GTTATTTGGT CGGTCGGCCT TCCCGGCTCG CGTCTTCACC
-------------------------------------------------------------------------------
7401  TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT TGCCGGGAAG
      AGGACGTTGA AATAGGCGGA GGTAGGTCAG ATAATTAACA ACGGCCCTTC
-------------------------------------------------------------------------------
7451  CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT TGTTGCCATT
      GATCTCATTC ATCAAGCGGT CAATTATCAA ACGCGTTGCA ACAACGGTAA
-------------------------------------------------------------------------------
7501  GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG
      CGATGTCCGT AGCACCACAG TGCGAGCAGC AAACCATACC GAAGTAAGTC
-------------------------------------------------------------------------------
7551  CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA
      GAGGCCAAGG GTTGCTAGTT CCGCTCAATG TACTAGGGGG TACAACACGT
-------------------------------------------------------------------------------
```

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7601  AAAAAGCGGT TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG
      TTTTTCGCCA ATCGAGGAAG CCAGGAGGCT AGCAACAGTC TTCATTCAAC
-------------------------------------------------------------------------------
7651  GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA ATTCTCTTAC
      CGGCGTCACA ATAGTGAGTA CCAATACCGT CGTGACGTAT TAAGAGAATG
-------------------------------------------------------------------------------
7701  TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG TACTCAACCA
      ACAGTACGGT AGGCATTCTA CGAAAAGACA CTGACCACTC ATGAGTTGGT
-------------------------------------------------------------------------------
7751  AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC TTGCCCGGCG
      TCAGTAAGAC TCTTATCACA TACGCCGCTG GCTCAACGAG AACGGGCCGC
-------------------------------------------------------------------------------
7801  TCAATACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT
      AGTTATGCCC TATTATGGCG CGGTGTATCG TCTTGAAATT TTCACGAGTA
-------------------------------------------------------------------------------
7851  CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC TTACCGCTGT
      GTAACCTTTT GCAAGAAGCC CCGCTTTTGA GAGTTCCTAG AATGGCGACA
-------------------------------------------------------------------------------
7901  TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA
      ACTCTAGGTC AAGCTACATT GGGTGAGCAC GTGGGTTGAC TAGAAGTCGT
-------------------------------------------------------------------------------
7951  TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG GAAGGCAAAA
      AGAAAATGAA AGTGGTCGCA AAGACCCACT CGTTTTTGTC CTTCCGTTTT
-------------------------------------------------------------------------------
8001  TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA ATACTCATAC
      ACGGCGTTTT TTCCCTTATT CCCGCTGTGC CTTTACAACT TATGAGTATG
-------------------------------------------------------------------------------
8051  TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA TTGTCTCATG
      AGAAGGAAAA AGTTATAATA ACTTCGTAAA TAGTCCCAAT AACAGAGTAC
-------------------------------------------------------------------------------
8101  AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA TAGGGGTTCC
      TCGCCTATGT ATAAACTTAC ATAAATCTTT TTATTTGTTT ATCCCCAAGG
-------------------------------------------------------------------------------
8151  GCGCACATTT C
      CGCGTGTAAA G
-------------------------------------------------------------------------------
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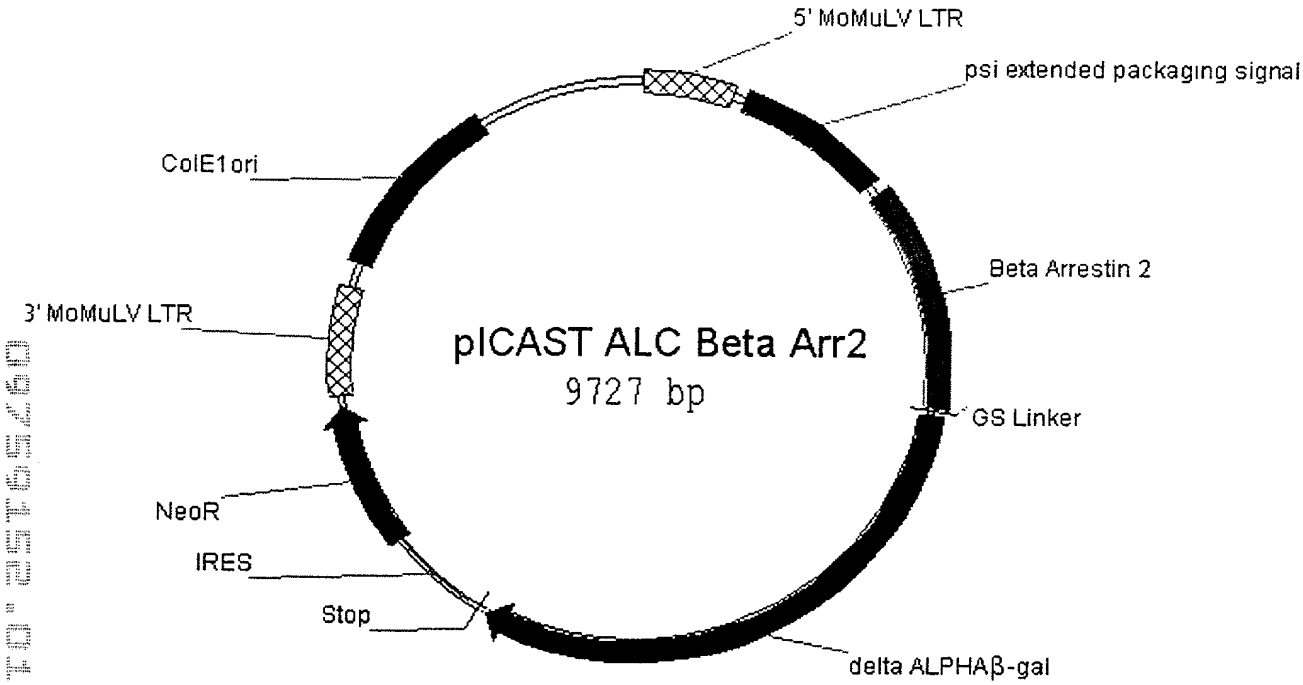

5' MoMuLV LTR
psi extended packaging signal
ColE1 ori
Beta Arrestin 2
3' MoMuLV LTR
pICAST ALC Beta Arr2
9727 bp
GS Linker
NeoR
IRES
Stop
delta ALPHAβ-gal

Figure 14

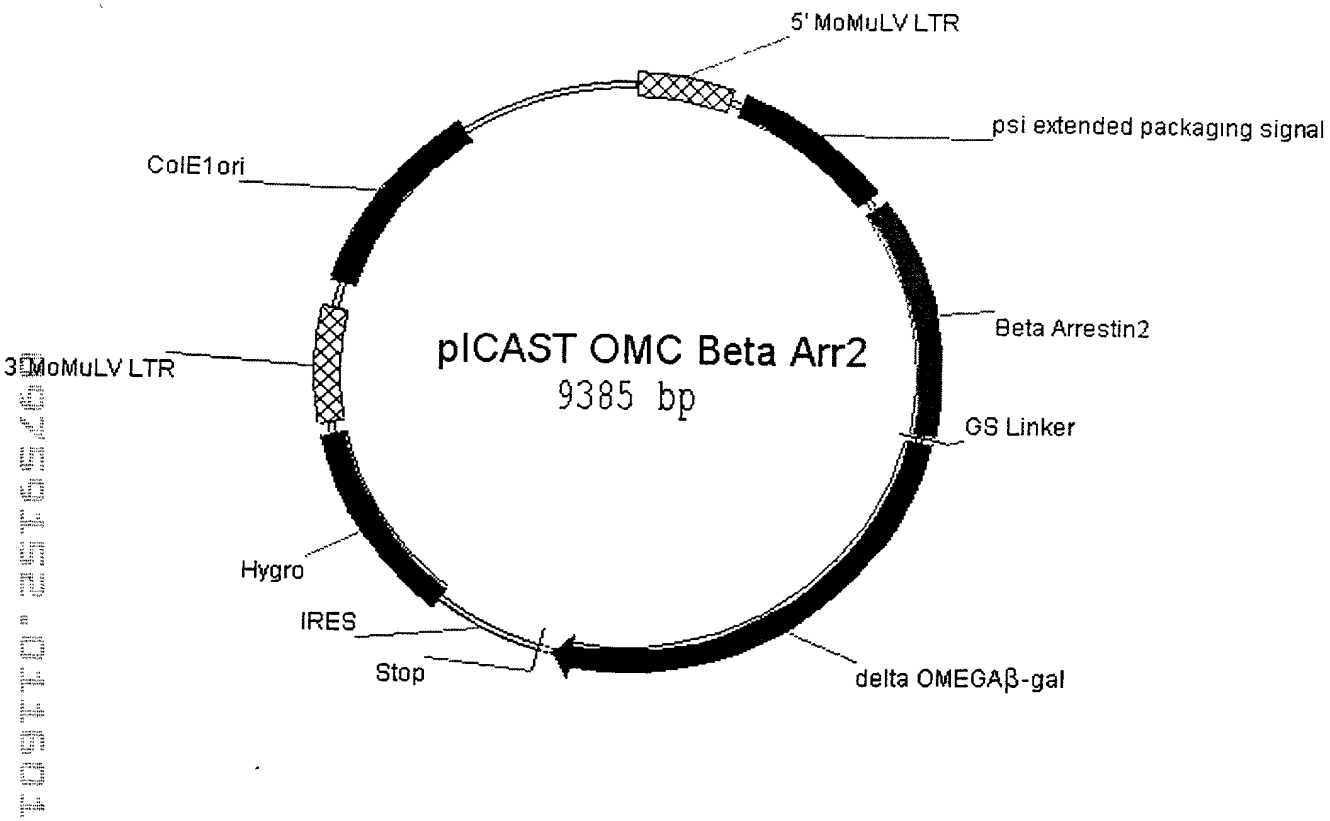

5' MoMuLV LTR
psi extended packaging signal
ColE1 ori
Beta Arrestin2
pICAST OMC Beta Arr2
9385 bp
3' MoMuLV LTR
GS Linker
Hygro
IRES
Stop
delta OMEGAβ-gal

Figure 15

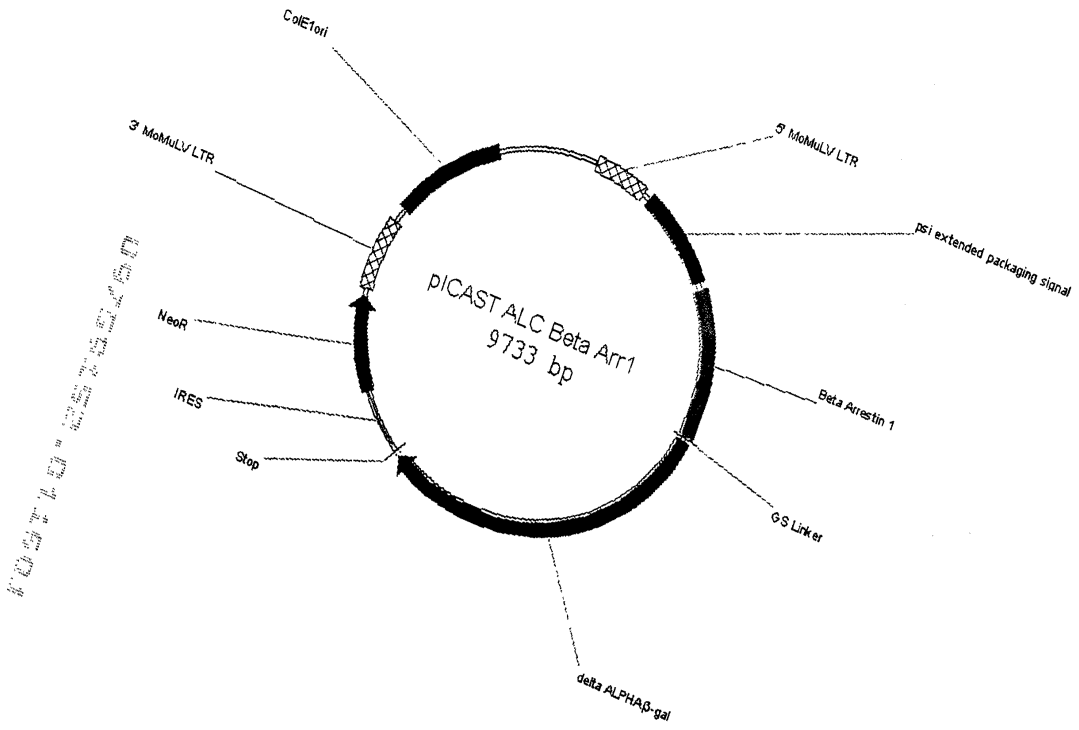

ColE1ori
3' MoMuLV LTR
5' MoMuLV LTR
psi extended packaging signal
pICAST ALC Beta Arr1
9733 bp
NeoR
IRES
Stop
Beta Arrestin 1
GS Linker
delta ALPHAβ-gal

Figure 16

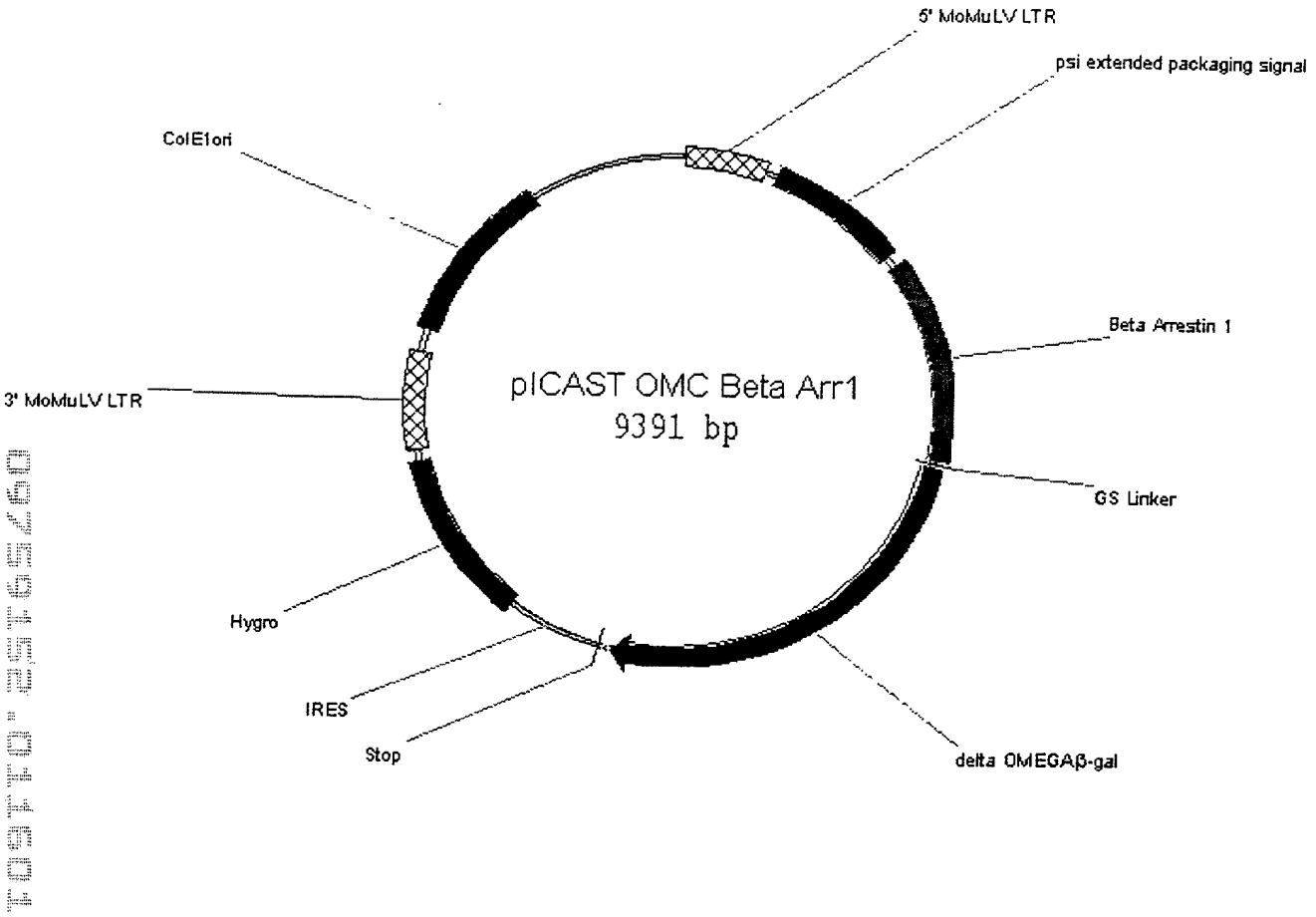

5' MoMuLV LTR
psi extended packaging signal
ColE1ori
Beta Arrestin 1
3' MoMuLV LTR
pICAST OMC Beta Arr1
9391 bp
GS Linker
Hygro
IRES
Stop
delta OMEGAβ-gal

Figure 17

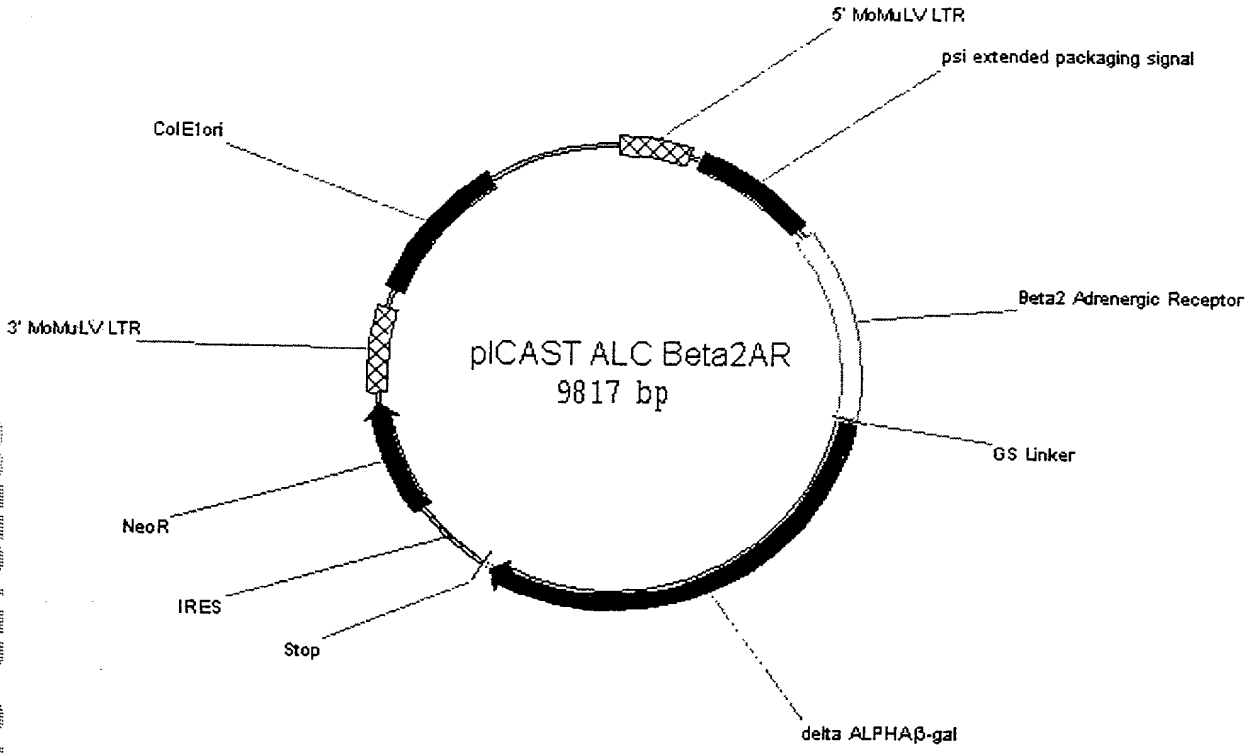

5' MoMuLV LTR
psi extended packaging signal
ColE1ori
Beta2 Adrenergic Receptor
3' MoMuLV LTR
pICAST ALC Beta2AR
9817 bp
GS Linker
NeoR
IRES
Stop
delta ALPHAβ-gal

Figure 18

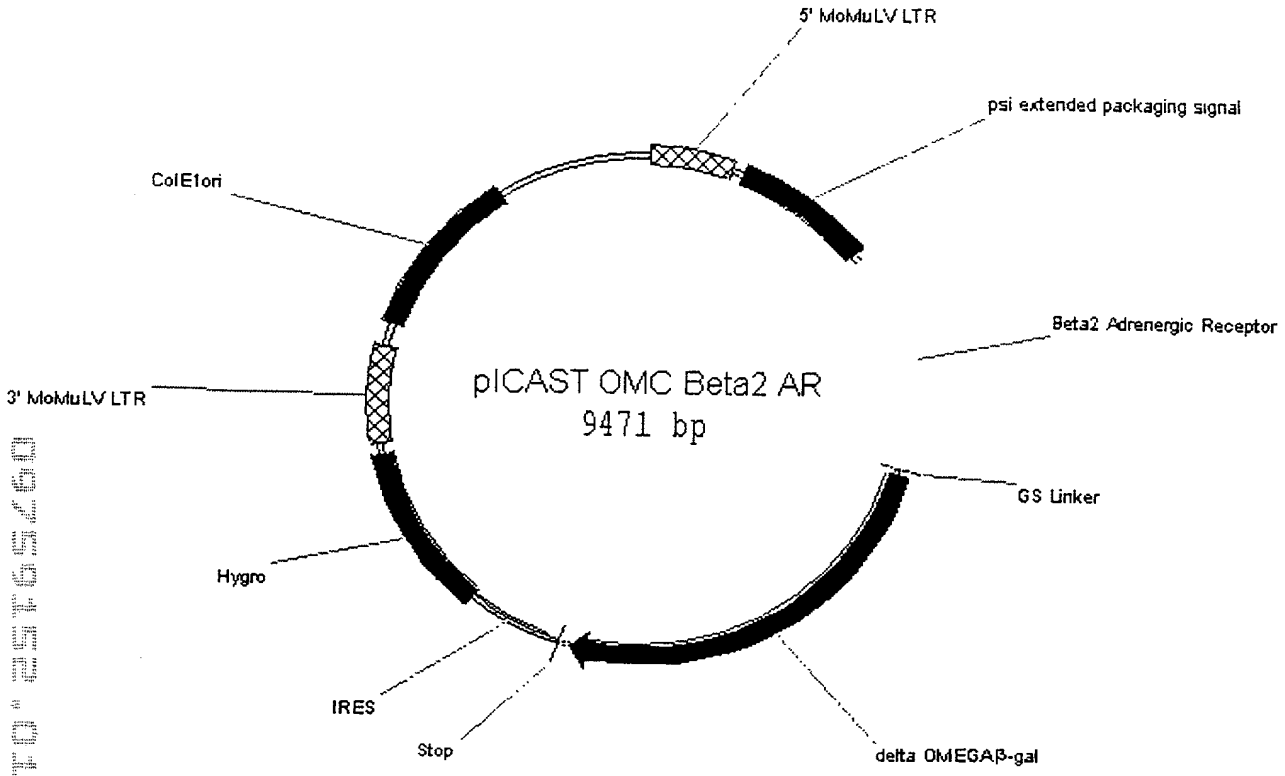

5' MoMuLV LTR
psi extended packaging signal
ColE1ori
Beta2 Adrenergic Receptor
3' MoMuLV LTR
pICAST OMC Beta2 AR
9471 bp
GS Linker
Hygro
IRES
Stop
delta OMEGAβ-gal

Figure 19

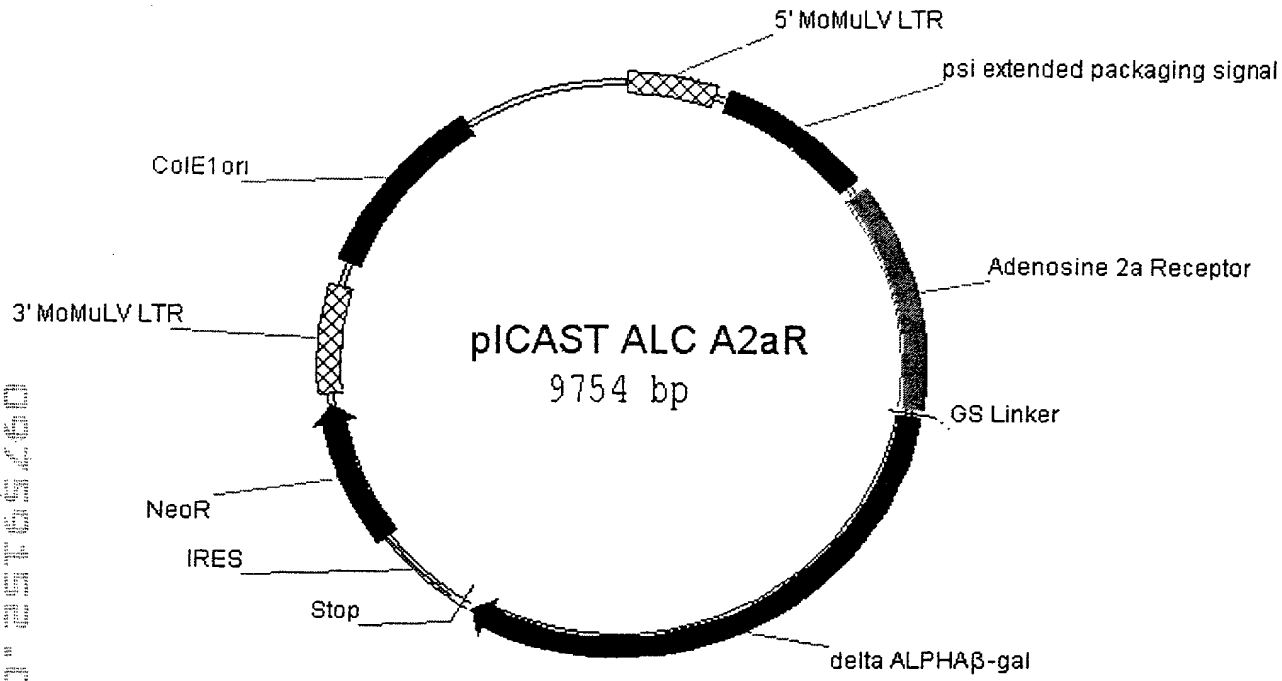

5' MoMuLV LTR
psi extended packaging signal
ColE1 ori
Adenosine 2a Receptor
3' MoMuLV LTR
pICAST ALC A2aR
9754 bp
GS Linker
NeoR
IRES
Stop
delta ALPHAβ-gal

Figure 20

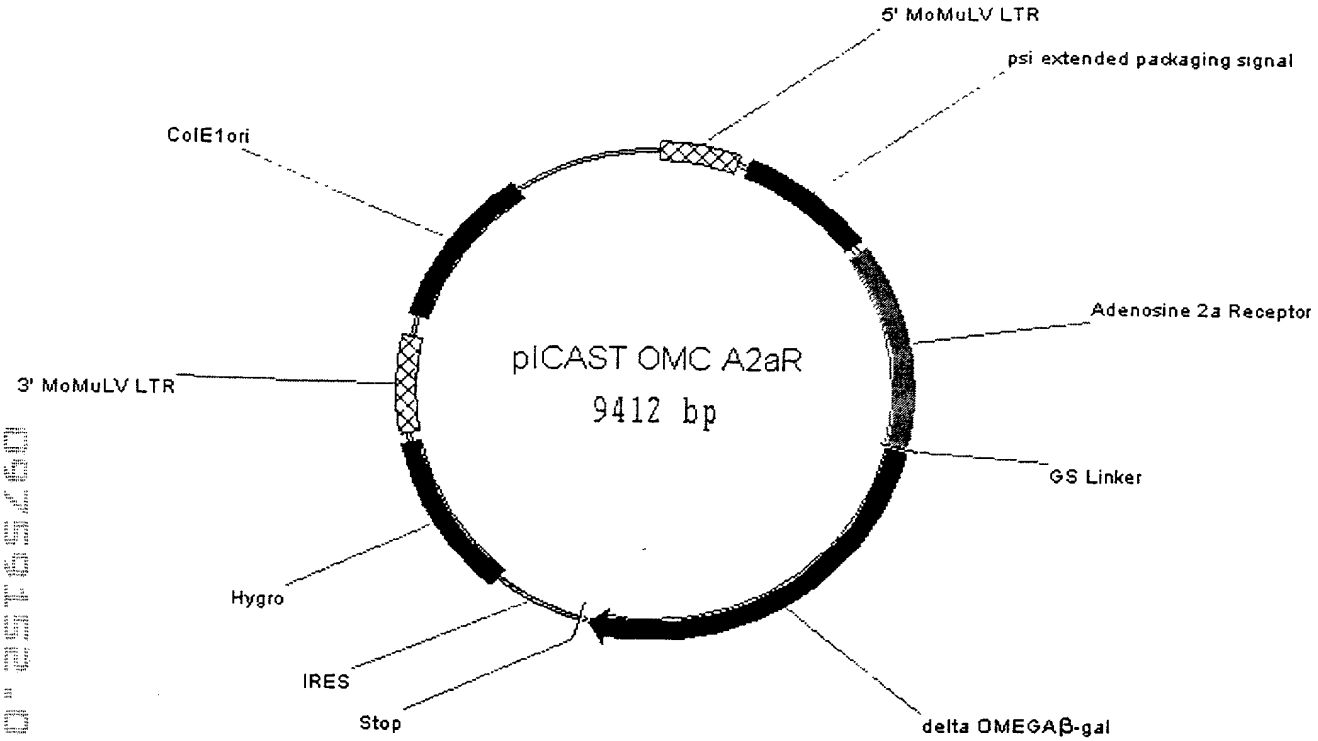

5' MoMuLV LTR
psi extended packaging signal
ColE1ori
Adenosine 2a Receptor
pICAST OMC A2aR
9412 bp
3' MoMuLV LTR
GS Linker
Hygro
IRES
Stop
delta OMEGAβ-gal

Figure 21

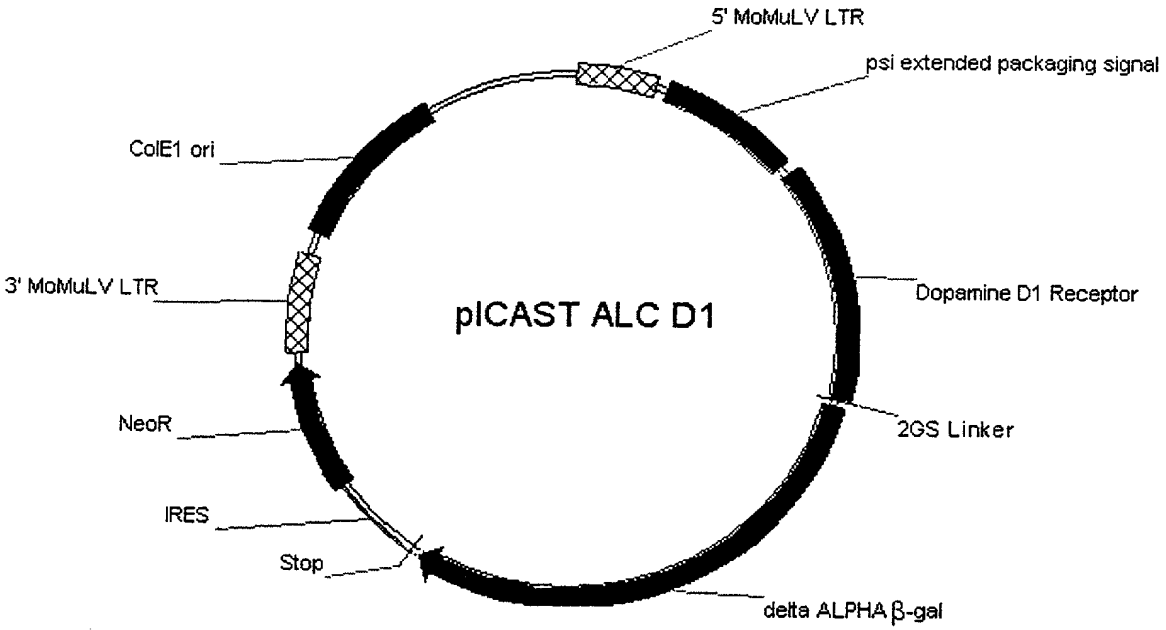
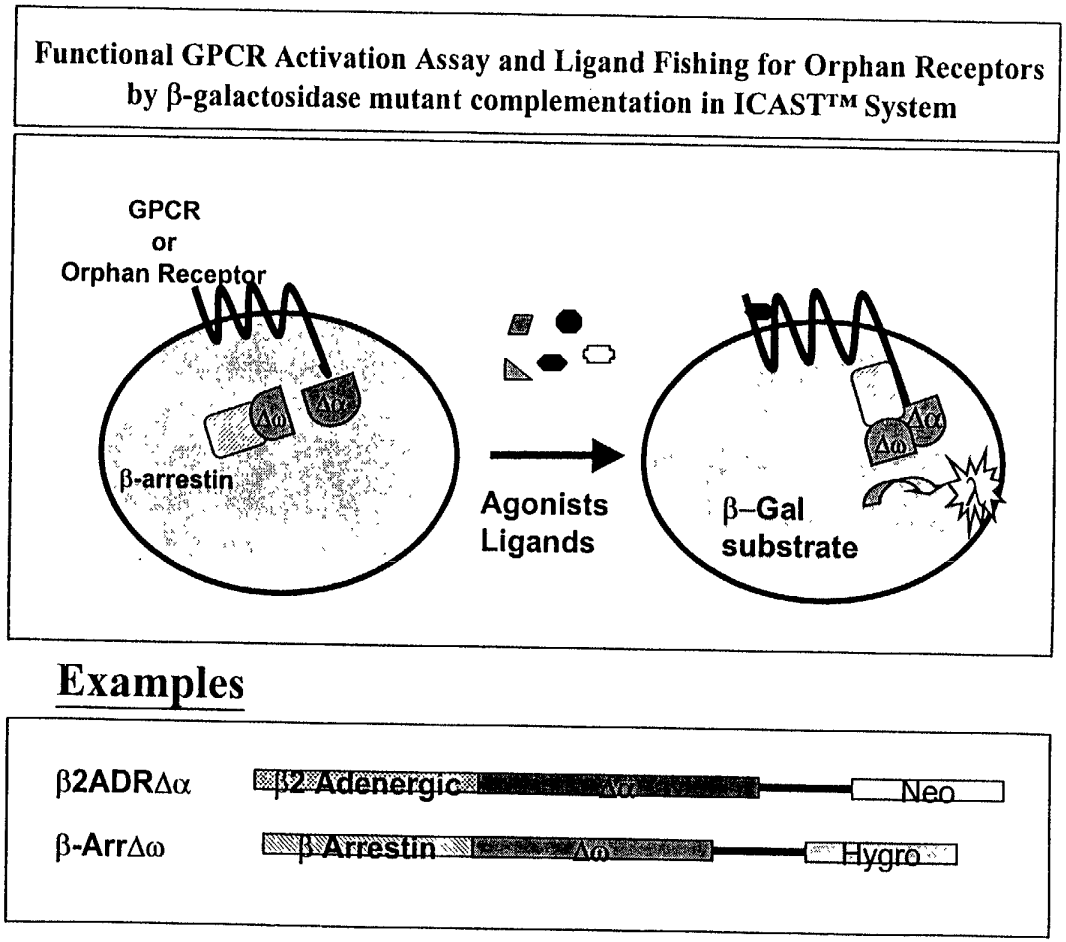
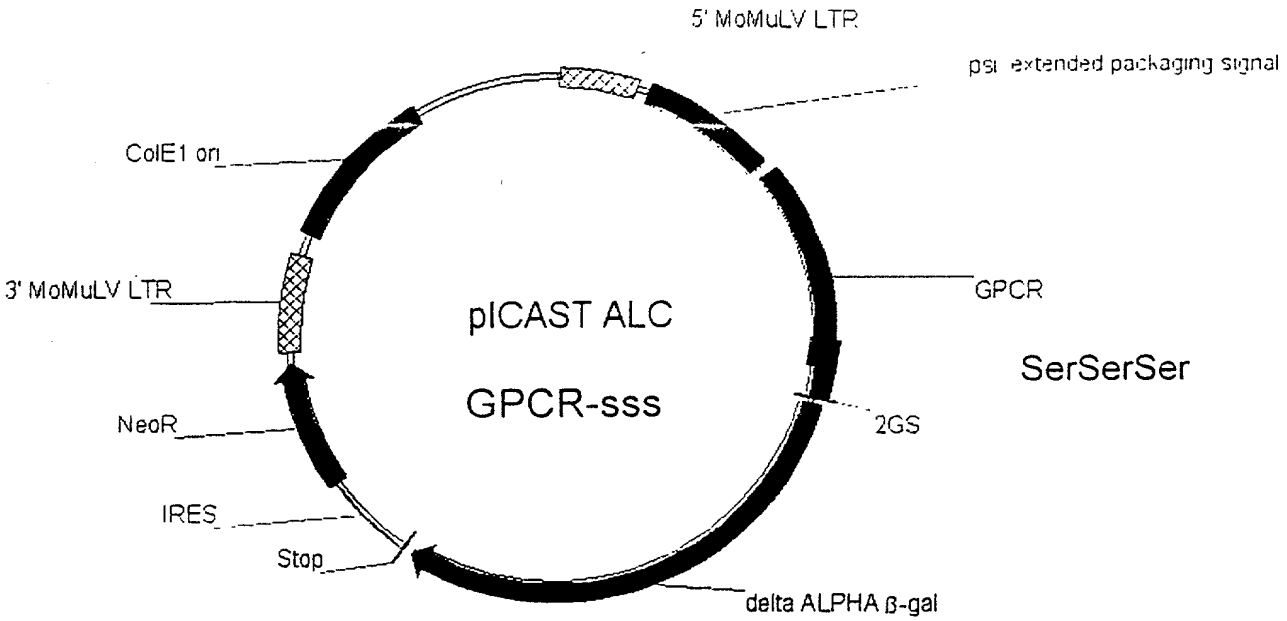

5' MoMuLV LTR
psi extended packaging signal
ColE1 ori
3' MoMuLV LTR
pICAST ALC D1
Dopamine D1 Receptor
NeoR
2GS Linker
IRES
Stop
delta ALPHA β-gal

Figure 22

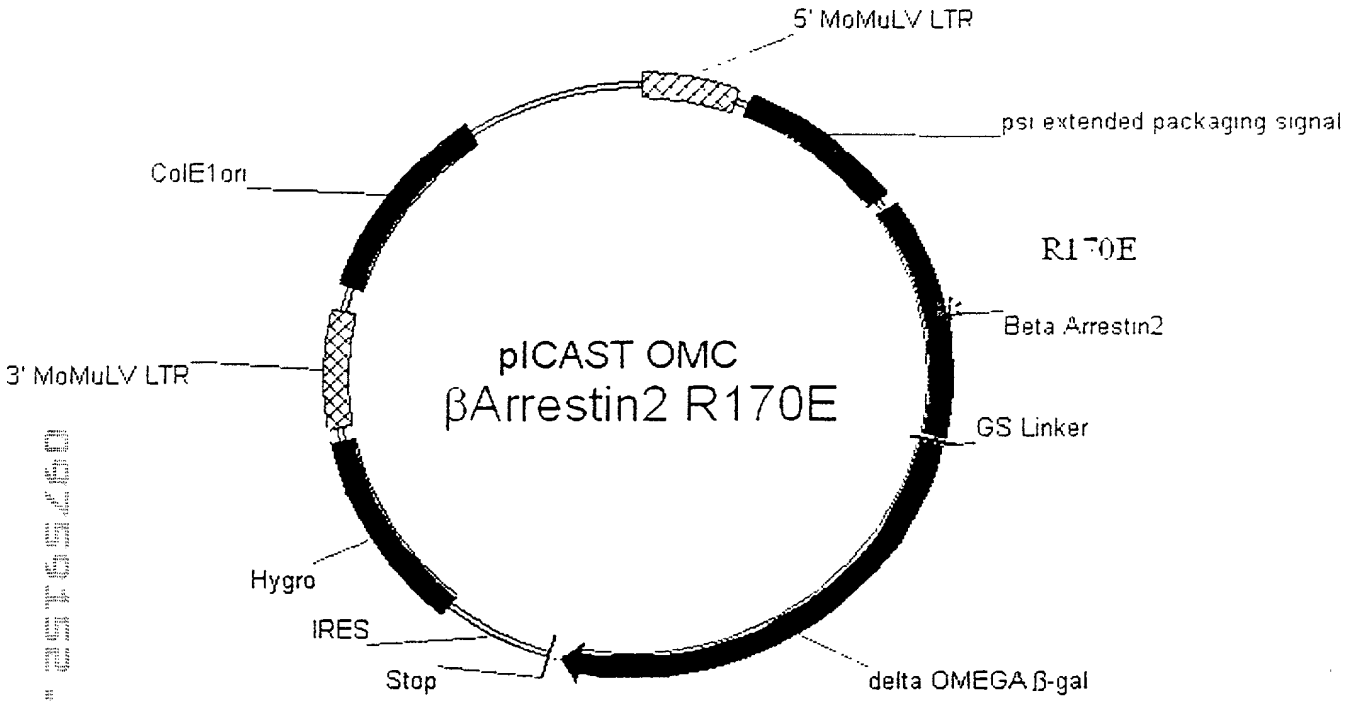
Figure 23


Functional GPCR Activation Assay and Ligand Fishing for Orphan Receptors by β-galactosidase mutant complementation in ICAST™ System
GPCR
or
Orphan Receptor
β-arrestin
Agonists
Ligands
β–Gal
substrate
Examples
β2ADRΔα
β2 Adenergic
Neo
β-ArrΔω
β Arrestin
Hygro



Vector for Expression of a GPCR with inserted Seronine/Threonine amino acid sequences as a fusion with β-gal Δα.

FIGURE 24



Vector for Expression of mutant (R170E) β-arrestin2 as a fusion with β-gal Δω.

FIGURE 25

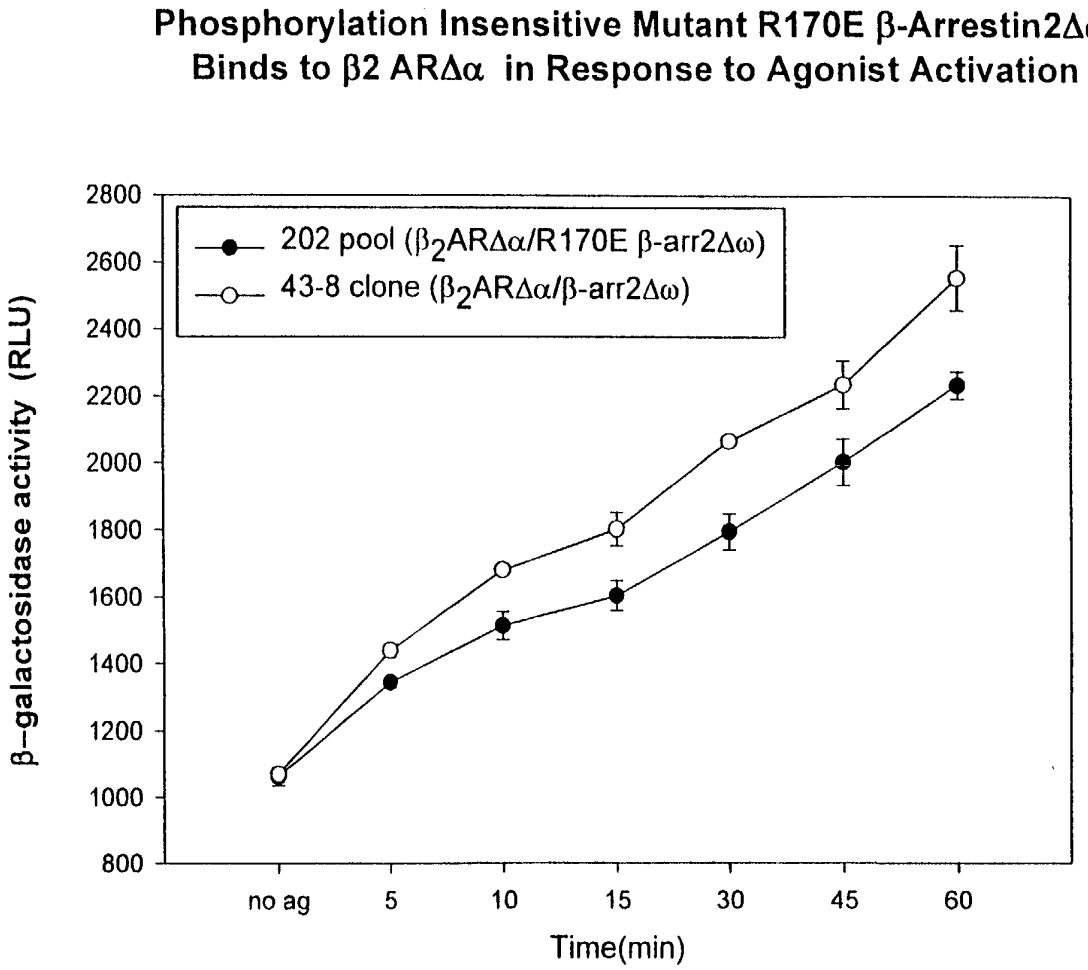
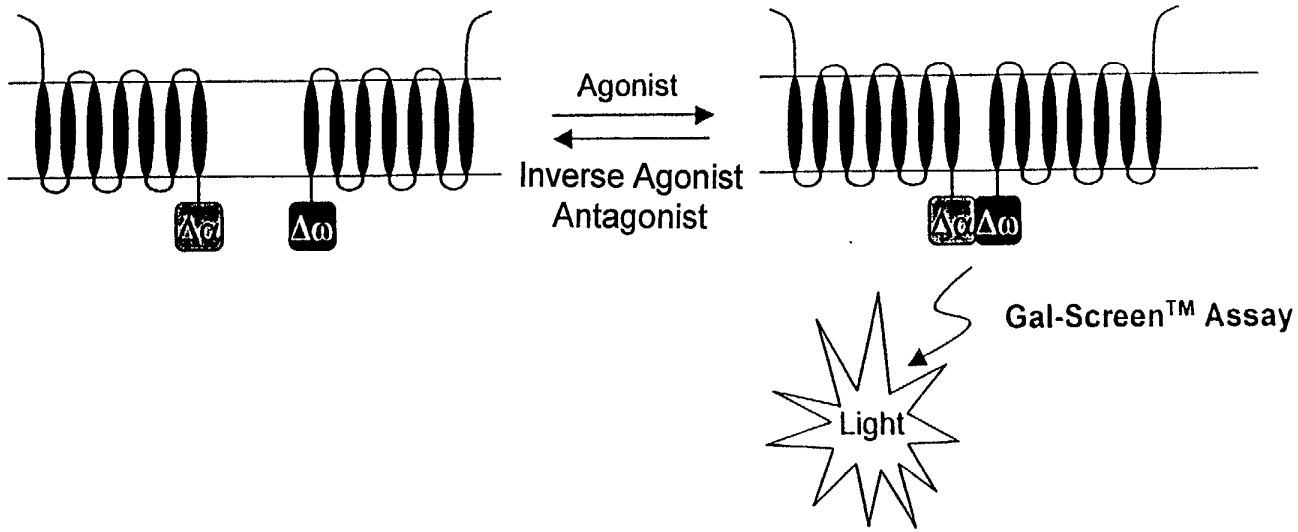

Phosphorylation Insensitive Mutant R170E β-Arrestin2Δω
Binds to β2 ARΔα in Response to Agonist Activation
202 pool (β2ARΔα/R170E β-arr2Δω)
43-8 clone (β2ARΔα/β-arr2Δω)
β–galactosidase activity (RLU)
2800
2600
2400
2200
2000
1800
1600
1400
1200
1000
800
no ag
5
10
15
30
45
60
Time(min)

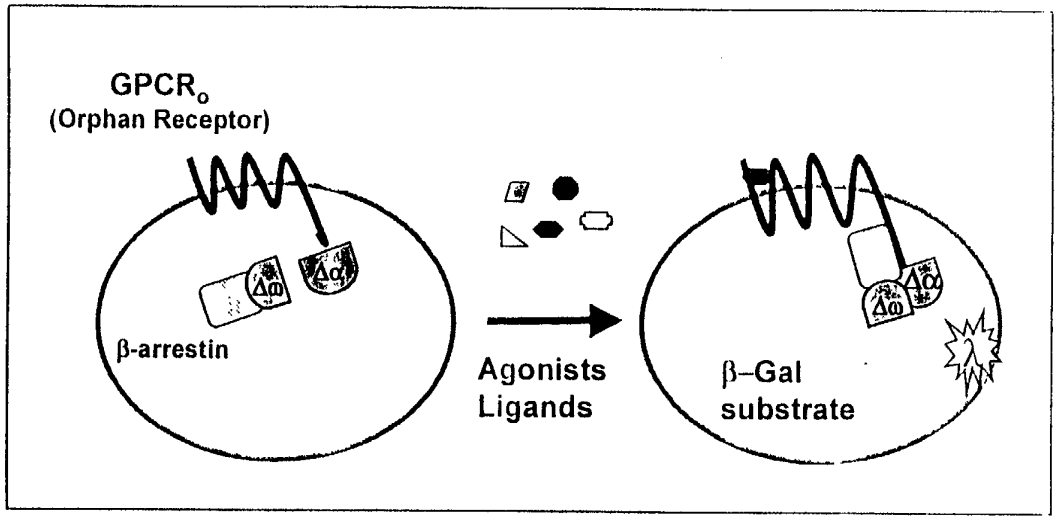
FIGURE 26

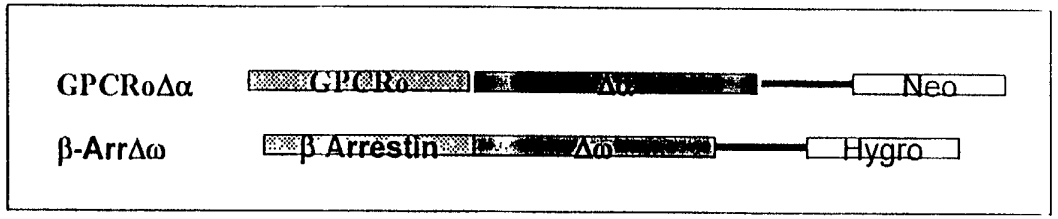


GPCR dimerization measured by β-gal complementation

FIGURE 27

Example-





Ligand Fishing for Orphan Receptors by β-galactosidase mutant complementation in ICAST™ System

FIGURE 28